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Understory ingrowth mortality model for black spruce (Picea mariana (Mill.) B.S.P.) in mixed species stands of boreal Ontario

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UNDERSTORY INGROWTH MORTALITY MODEL FOR BLACK SPRUCE [*Picea mariana* (Mill.) B.S.P.] IN MIXED SPECIES STANDS OF BOREAL ONTARIO

by

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W. R. ANDREW INNERD

A CAUTION TO THE READER

This M.Sc.F. thesis has been through a formal process of review and comment by three faculty members and an external examiner. It is made available for loan by the Faculty of Forestry and Forest Environment for the purpose of advancing the practice of professional and scientific forestry.

The reader should be aware that opinions and conclusions expressed in this document are those of the student and do not necessarily reflect the opinions of either the thesis supervisor, the faculty or Lakehead University.

ABSTRACT

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An individual tree mortality model was developed for understory ingrowth mixed species stands of boreal Central Ontario. Data for the model came from long-term permanent sample plots initiated by the AmericanCan and Kimberly Clark Corporations and now maintained by the Ontario Ministry of Natural Resources. The model took the form of a logistic regression equation. Tree size, stand density and basal area were found to be variables of particular importance, perhaps because they most directly reflect the situation of the tree within its particular system. Also significant was average stand dbh and ingrowth density. The model correctly predicted 45% of the observed mortality and 70% of the observed survival in the data set used to develop the model. For the independent data set the model was able to correctly classify 30% of the observed mortality and 66% of the observed survival. Future research efforts into mortality should include data collection on the causes of mortality and the interaction of a particular tree with its environment.

Key Words: mixed species, boreal, Ontario, mortality, logistic, understory, ingrowth, black spruce

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1 INTRODUCTION

1.1 STUDY PROBLEM

There are at least two reasons for modelling mortality of understory ingrowth individuals. First, behaviour of trees in a sub-canopy position is not well understood; there is a scientific knowledge gap. As such, there is a limited understanding of how mixedwood stands develop and the succession that might take place. Second, a better understanding of understory stand dynamics can lead to better growth and yield models. As dynamic, complex entities, forests of today are not forests of tomorrow. An increased knowledge of understory ingrowth dynamics can lead to improved decision support tools.

A growth and yield model is used to predict volume, annual allowable harvest, future stand composition, tree sizes and more. Better models lead to a better understanding of how stands and forests behave, greater accuracy of prediction, and increase the confidence of model users. An increase in scientific knowledge of forest stand dynamics leads to better growth and yield models that incorporate those dynamics. As decision support tools, such models are well suited to providing information on future stand conditions. If mortality were ignored in a growth and yield simulator, unreasonable and unworkable assumptions of constant stocking, unchanging structure and constant composition would be made. Accounting for mortality leads to better models because stocking, structure and composition are allowed to vary.

As forest stands undergo succession their properties change. The properties of interest might include, for example: species composition, net merchantable volume (NMV) and habitat suitability. If NMV is the property of interest then a growth and yield model capable of accurately predicting a stand's NMV for an extended period of time is a valuable tool to resource managers because stand volume is not constant and changes over time. For example, when canopy trees die and are replaced by individuals from the understory, stand volume changes. A mortality model of understory ingrowth is thus an important component of a growth and yield model because over time, understory trees grow and replace canopy trees.

When an individual-tree mortality model is developed for a single species the expectation is that the species behaves in a uniform manner, regardless of origin or age, and, therefore, acts as a 'block' or platform from which an investigation of mortality can develop, however, for a given species, the understory and the overstory will behave differently. Many mortality modelling efforts deal with even-aged, single species stands and definitions of regular and irregular mortality (Lee 1971) are for such stands. It is, therefore, necessary to examine mixed species, multi-aged stands. Is it possible to model understory mortality in a distinct fashion from overstory, and if so, what are the tree, species, and stand characteristics, indicative of mortality for individual-trees? Presumably, conditions created by a canopy cause sub-canopy individuals to incur unique adaptations to the conditions, and thus survival pathways are different relative to pathways of canopy individuals.

Presented within this thesis is an individual-tree mortality model for black spruce [*Picea mariana* (Mill.) B.S.P.] species in Northern Ontario. The model is for ingrowth trees, located in the understory of mixed-species, multi-aged stands. The model takes

the form of a logistic regression equation. The intent is to model a specific component of stand structure and show that stand structure is inherently important to, survival and mortality, of black spruce. As such, stand structure must be accounted for when modelling black spruce mortality. In turn, this has potential to lead to better growth and yield models.

1.2 STUDY OBJECTIVES, OUTLINE AND LIMITATIONS

The primary objective of this thesis is to develop a mortality model capable of predicting black spruce understory ingrowth mortality. The second objective is to develop a better understanding of forest stand dynamics. These two objectives are to be met by development of a mortality model incorporating tree, species and stand attributes into a single model.

The Literature Review and Theoretical Background provides introductory material on mortality and mortality modelling, including previous mortality modelling efforts found in the literature. The Methods and Materials section provides information on the actual procedure used to develop the model presented in this thesis, as well as information on the two data sets used. The Results and Discussion section outlines in detail the developed model and the major findings, along with significance of the findings. Finally, in the Conclusion pertinent results are highlighted.

This study was undertaken with the use of long-term historical data sets. Such data sets cannot be collected during the course of a Master's degree due to time and money constraints. As a result, when using such data sets, the contents are received in an "as is" condition, and neither lack of data nor quality of data is reproachable.

A further limitation of the thesis as regards the data sets is that it was not possible to determine if the stands in which the sample plots were located were mixedwood stands, as defined by the OMNR (2000), or otherwise. It was only possible to determine that plots were located in mixed species stands (see sections 2.1.2 and 2.2.5.3 for more information).

2 LITERATURE REVIEW AND THEORETICAL BACKGROUND

2.1 BLACK SPRUCE AND MIXEDWOOD ECOLOGY

2.1.1 Black Spruce

In Canada black spruce [*Picea mariana* (Mill.) B.S.P.] is one of the most common tree species in the Boreal forest. Black spruce grows in a cold climate with a humid to subhumid moisture regime (Viereck and Johnston 1990). It is found on a variety of soils including wet organic, deep humus, clays, loams, sands, coarse till, boulder pavement, shallow soil mantles over bedrock, peat bogs and swamps (Viereck and Johnston 1990).

On organic soils, black spruce is most commonly found in pure stands, while on mineral soils it is most commonly found in mixed stands commonly associating with white birch [*Betula papyrifera* Marsh.], trembling aspen [*Populus tremuloides* Michx.], jack pine [*Pinus banksiana* Lamb.], white spruce [*Picea glauca* (Moench) Voss], tamarack [*Larix laricina* (Du Roi) K. Koch], and balsam fir [*Abies balsamea* (L.) Mill.] (Viereck and Johnston 1990). Black spruce is found on lower quality sites with lower soil fertility than white spruce, which is generally more site demanding, although white spruce also grows on extremely diverse sites (Nienstaedt and Zasada 1990).

Underneath a canopy, black spruce develops in as little as 10% full sunlight intensity (Viereck and Johnston 1990). Suppressed black spruce has limited ability to respond to release because it develops a limited crown (Viereck and Johnston 1990).

Over time black spruce replaces trembling aspen, white birch and jack pine (Viereck and Johnston 1990).

The known prevalence of widespread and reoccurring events such as eastern spruce budworm (*Choristoneura fumiferana* (Clem.)) in the data makes modelling black spruce mortality difficult. This is because an event such as a spruce budworm outbreak may not be terminal to black spruce. It may, however, affect characteristics of trees and stands. This is important to recognize because cause of death from such events is not related to competition or suppression, and, as such, cause of mortality within a data set is confounded (see section 2.2.2 for more information).

2.1.2 Boreal Mixedwoods and Mixed Species Boreal Forests

It is important here to make a distinction between a boreal mixedwood stand as defined by the OMNR (2000) and a mixed species boreal stand as defined within this thesis. A **boreal mixedwood site** (OMNR 2000) is:

> "an area with climatic, topographic and edaphic conditions that favour the production of closed canopies dominated by the five boreal mixedwood site defining tree species, which are trembling aspen or white birch in early successional stages, black spruce or white spruce in mid-successional stages and balsam fir in late successional stages."

Typically boreal mixedwood sites have soils that are deep, well-drained and fertile with medium to fine texture on mid-slope positions, and exclude wet lowlands, dry sand plains and shallow soils on bedrock outcrops (McClain 1981, OMNR 2000).

A **boreal mixedwood stand** (OMNR 2000) is: "a tree community on a boreal mixedwood site in which no species exceeds 80% of the basal area." Species normally found in boreal mixedwood stands include jack pine, white pine [*Pinus strobus* L.], red pine [*Pinus resinosa* Ait.], eastern white cedar [*Thuja occidentalis* L.], tamarack,

largetooth aspen [*Populus grandidentata* Michx.], balsam poplar [*Populus balsamifera* L.], white elm [*Ulmus americana* L.], black ash [*Fraxinus nigra* Marsh.] and black willow [*Salix nigra* Marsh.] (OMNR 2000).

In this thesis, which examines mortality in mixed species boreal stands, the precise definitions of site type and stand composition are less important. It was not possible to define stands in which plots were located as being boreal mixedwoods. As a result, it is only possible to say within this thesis that mixed species stands were examined.

Stand structural diversity occurs when trees of distinctly different heights, of any species, exist within a stand in direct proximity to each other. At least one layer of trees exists underneath the canopy. An understory individual occurs in a structurally complex stand and such an individual exists below the canopy. For the purpose of this thesis, an ingrowth individual is defined as a tree not present as a member of a permanent sample plot in a previous measurement period. Thus, an ingrowth individual does not exist until at least the second plot measurement. An individual tree present below the canopy and that meets the requirements of the ingrowth definition is an understory ingrowth tree.

Behaviour of understory ingrowth individuals is distinct from individuals which are not understory or ingrowth. As such, their development is distinct and it is worth examining their functioning in an explicit manner. Within this thesis, understory ingrowth trees in structurally complex mixed species boreal stands are examined.

2.2 INDIVIDUAL TREE MORTALITY

2.2.1 Mortality in Empirical Data Sets

The ability to view individual tree mortality is limited. Inconveniently, tree mortality is rarely observed in any direct manner. Causes of tree mortality are rarely included in empirical survey data that mortality modellers almost universally rely on. This reduces observation of mortality to presence or absence of life after a set period of time. A first step in modelling mortality is to clearly define tree mortality.

A general definition of tree mortality would be to regard it as the absence of life processes for an individual tree with preclusion of life processes taking place in the future. A dead tree does not conduct, and is not capable of conducting, processes normally associated with a living tree, including, but not limited to, photosynthesis and respiration. In most studies when tree mortality is detected via survey data, it is only the observed absence of life that is recorded; cause of mortality is distinctly absent in any explicit manner. In consequence, only implicit mortality is modelled and modellers are propelled to examine the implicit explanation of mortality. The implicit implication assumed of the data is nearly always that death was induced by competition or suppression.

2.2.2 Causal Agents of Tree Mortality

A tree dies from any of a variety of biotic or abiotic factors, which may be termed causal agents, and these agents occur during one or more events and act individually or conjointly to induce death. Causal agents of mortality need not be external to the tree; they may be an inherent component of the tree, as a function of the

tree or as properties of the tree species. This is related to fitness, genetic makeup, or suitability of a particular tree or species to a specific micro-site. A mortality event is a period during which one or more causal agents act upon a tree to induce death. It may be discrete (occurring in a single instance) or continuous (occurring over a period of time) and for a particular tree there may be more than one such event.

The susceptibility of a tree in conjunction with the duration and intensity of actions on a tree in the form of causal agents determines when a tree dies (Waring 1987). In general, a tree dies when it cannot acquire or mobilize sufficient resources to heal injuries or otherwise sustain life (Waring 1987).

Growth and yield data sets generally do not contain explicit causes of an individual tree's death, however, cause or causes of death may be implicitly contained in the data. That is to say, a dead tree may have died from causes that were captured as expressed characteristics of the tree and/or the stand in which it existed, and are thus implicitly contained within the data. Attempting to model death of a tree based on implicit characteristics of death is an effort based on tree, tree species and stand behaviour.

As states, life and death are absolute. There is no ambiguity; either a tree is alive or it is dead. Transition from a living state to a dead state is unidirectional and discrete. A living tree may be dying while it is alive but a dead tree is simply dead. Alive and dead are states; they are mutually exclusive. It is not possible for a tree to be alive and dead at the same time because for an individual tree, life and death are mutually exclusive.

In modelling forest progression through time, an error in favour of tree survival can be corrected at a later stage of modelling. This is because survival as a state is

transient, and, therefore, does not suffer from Markovian termination, which is the situation whereby an individual within a system being iteratively modelled is not considered, for any reason, after an increment of the model. Conversely, a mortality error cannot be corrected at a later stage of simulation, because mortality as a state is absorptive; death is absolute.

2.2.3 Variables

Many variables have been used to model the mortality of individual trees. They include (e.g., Lee 1971, Hamilton and Edwards 1976, Monserud 1976, Buchman et al. 1983, Hamilton 1986, Monserud and Sterba 1999, Hawkes 2000, Eid and Tuhus 2001, Fridman and Stahl 2001, Hann and Hanus 2001, Yao et al. 2001, Bigler and Bugmann 2003, Jutras et al. 2003, Yang et al. 2003):

- tree size (dbh, dbh^2, dbh^{-1}, height),
- stand density,
- individual tree competition,
- stand composition,
- tree growth (e.g. vigour expressed as diameter increment or height change),
- crown size,
- ratio of crown height to tree height,
- clear bole length,
- age,
- social position,
- stand basal area,

- percent defect,
- length of growing period,
- site conditions and productivity (site indices),
- competition indices,
- geographical location,
- mean stand dbh,
- basal area of large or larger trees,
- individual tree proportion of basal area,
- basal area of larger broadleaf trees,
- basal area of taller trees, and
- stochastic events such as hail, fire and wind.

Factors found important in predicting mortality appear to be largely circumstantial. Data availability, time and experience have all played a role in model development. Burkhart (2003) states that the pattern in a dataset is often described with a relatively simple model, and that patterns usually depend on a few main causal factors that are summarized readily. Predictive ability of a model tends to peak rather quickly ('Ockham's Hill') and then decrease with increasingly complex models (Gauch 1993).

2.2.4 Mortality

Mortality as a component of growth and yield is key to accurate predictions of stand composition, growth, structure, and volume (Lee 1971, Hamilton and Edwards 1976, Monserud 1976, Hamilton 1986, Yang and Titus 2002). It is also an important component of forest stand dynamics (Bigler and Bugmann 2003, Jutras et al. 2003, and

Yang et al. 2003). Whether the perspective is growth and yield, stand dynamics or succession, an examination of tree mortality enables a better understanding of past, present, and future stand compositions (Buchman et al. 1983).

While some models examine individual tree mortality in mature, even-aged stands (e.g., Hamilton and Edwards 1976, Monserud and Sterba 1999, Yao et al. 2001, Yang et al. 2003), few examine juvenile mortality (e.g., Kobe and Coates 1996), or looked directly at understory ingrowth mortality in structurally and compositionally complex stands. Lundqvist (1995) simulated sapling population dynamics in uneven-aged, single species forests but did not examine mixed-species stands or explain possible causes of mortality. Boreal mixedwood stands are more complex and dynamic than other boreal forest types (Chen and Popadiouk 2002). Because of this mixedwood forests need to be examined separately from even-aged and single species stands.

Mortality and survival predictions in a growth and yield simulator control stand density estimates, and, therefore, volume prediction because in individual tree simulators stand volume estimation is an aggregation of individuals (Leary 1980). Knowing which trees survive or die not only allows better management decisions (Yang and Titus 2002) but also permits a better understanding of tree, stand, and forest behaviour both with and without anthropogenic influences. It also helps predict future stand composition, however, predicting mortality of an overstory individual indicates what will not be present in the future canopy. A mortality prediction on its own does not predict future composition. An understory ingrowth mortality model has an additional advantage in that it also acts as a *defacto* recruitment model. As understory individuals grow, they become components of the canopy, and, because of this they are an important component in the prediction of future stand composition. The ability to predict change

is essential to forest planning so that species composition, stand structure and volume of forest stands are accurately assessed (Hamilton and Edwards 1976, Teck et al. 1996).

An examination of mortality is one means of examining stand dynamics. Change in forest composition is viewed as being governed by a set of inter-species rules that direct the progress of a forest through time (Harry and Smith 1980). As a means to an end, mortality modelling leads to rules that result in better growth and yield models, and a better understanding of the behaviour of the ecological system in question.

A predictive or explanatory mortality model must include elements of the system it represents (Burkhart 2003). A model that does not contain elements responsible for mortality will not model mortality with any degree of accuracy (Hawkes 2000). It is, therefore, of the utmost importance to accurately assess mortality in a data set, and identify variables associated with mortality and the potential application of the model as a component of a system. A basic assumption of mortality modelling is that live trees and dead trees have observable characteristics that make them separable (Monserud 1976).

Hawkes (2000) provides explanations for mortality of woody plants in the form of seven categories of mortality agents stemming from a review of literature concerning mortality. The seven categories are age, size, competition, carbon balance/growth, random, abiotic and multiple factors.

According to Hawkes (2000), age is used to explain mortality by assuming that a woody plant senesces and becomes less vigorous as it ages, with the result being a greater susceptibility to environmental stresses. In the second category, size is used to explain mortality because of interactions with age, competition, and the carbon balance of the woody plant. As Hawkes (2000) points out, size is a state, not a process, and,

therefore, limits the utility of size as a predictor over time. The problem with age and size as predictors of, or as explanations of mortality, is that neither age nor size is actually responsible for death, rather they are factors associated with the observation and rate of mortality.

The third proposed explanation of mortality is competition, whereby mortality is incurred because neighbouring trees or vegetation deprive an individual of resources necessary for life. Size is related to competition (Chen 2006), so tree size and competition experienced by an individual tree are important to examining mortality within a system.

The fourth category used to explain mortality is carbon balance and carbon growth. The category explains mortality by stipulating that once a plant can no longer synthesize carbon (for whatever reason) it will die; it is said to be a highly integrated predictor because age, size, abiotic factors, and competition all affect it. It is similar in perspective to competition-based mortality in that competition results in a lower or negative carbon balance. Carbon balance and carbon growth mortality requires an examination of a tree with more detailed information than is commonly found in growth and yield data sets.

The fifth category of mortality is random factors, which are used when cause of mortality is not known or is too complex to simulate. The problem with this as a factor or category of mortality is that most causal agents are unknown. In a growth and yield simulator this category could be used to reduce stand density without attributing a cause to the death.

The sixth category is abiotic and is used when an environmental abiotic factor, external to the plant, is assumed or observed to cause mortality (e.g., hail, drought, fire,

etc.). In this thesis, abiotic factors are further classified into irregular and catastrophic mortality, neither of which is further considered because they are either not observable with the available data or are confounded with the available data. Such a category is used to predict mortality for regular events such as spruce budworm attack when the regularity of attack is known with some level of certainty.

The seventh and final category explaining death, as proposed by Hawkes (2000) is multiple factors, which use two or more predictors to explain death. It is used when regular and irregular factors affect death. This approach is the obvious one to take when examining highly variable systems that may have multiple causal agents acting singly or in unison within the system and upon a tree.

Even with these seven categories it is difficult to explain mortality and predict its occurrence. Part of the problem is that little forensic mortality work has been conducted for tree mortality, and as previously discussed, direct and accurate information concerning precise cause of tree death is largely unavailable. Monserud and Sterba (1999) point out that a mortality modeller working with empirical data mostly hopes to capture average rate of mortality, and relate it to a few reliable and measurable size or site characteristics. For instance, Yang et al. (2003) noted that rate of mortality for juvenile trees is high, decreases with increasing size and then starts to increase again with a further increase in tree size. In order to model this observation they used diameter and diameter squared.

The problem with the use of size as a predictor variable is that it is not responsible for mortality (Vanclay 1994); it is merely associated with it. Tree size can be viewed as an integrated response of a tree to site quality and age, and, as such, tree size implicitly contains such site and age effects (Monserud and Sterba 1999). For a

particular site, two trees of the same age, species and genetic makeup should be the same size, *ceteris paribus*. Because of this, the usefulness of tree size as a variable is in relating the individual tree to its surroundings.

In order for a variable to have explanatory power it must in some way be associated with mortality (Hawkes 2000). For example, diameter increment is a commonly used variable to represent vigour (e.g., Yang et al. 2003). Diameter increment is important because within the postulated hierarchy of carbon allocation within a tree, a tree will allocate photosynthate to height growth and root development prior to diameter growth or to production of defensive compounds (Waring 1987). During a period of stress, such as drought or insect attack, a decrease in diameter increment is more immediately observable, whereas other tree variables such as height are less influenced (Waring 1987). Diameter increment is a highly responsive indicator of vigour or stress of a particular tree. A lack of diameter increment for a particular tree is expressive of a problem such as insufficient carbon accumulation, an imbalance between respiration and photosynthesis, environmental conditions unsuitable for growth, an inadequate root system and so on. A tree is stressed when it has trouble acquiring or mobilizing the necessary photosynthate for life. Although in an observational dataset cause of stress may be unknown it may be indirectly measurable as a function of stem diameter growth.

Environmental stress (i.e., lack of water, light deficiency, etc.) may affect sub-canopy trees differently than canopy trees. If an understory tree has a well-developed root system it may be less susceptible to drought than an overstory tree because it has lower requirements. Similarly, larger understory trees may be less likely to survive

during periods of stress than smaller understory trees because a smaller tree will have lower maintenance costs.

2.2.5 Defining Mortality

When modelling and classifying mortality, it is necessary to determine to what extent causality and regularities are taken into account, and what phenomena are regarded as stochastic (Alenius et al. 2003). Because of the numerous causes of mortality and the complexity of determining causal agents, mortality is generally regarded as being regular or irregular (Lee 1971). Lee (1971) describes regular mortality as mortality that occurs when trees grow so close together that they compete for survival and irregular mortality as being tree death caused by insect attack, disease, windfall, fire or snow damage. More generally, regular mortality according to Lee (1971) is competition induced and irregular mortality is otherwise incurred.

In order to understand tree mortality within the context of an empirical modelling effort based on a long-term remeasured data set, definitions of the types of mortality inherent to such a system need to be more clearly defined than originally proposed by Lee (1971). This is especially the case in this thesis, since Lee (1971) was largely dealing with even-aged single species stands and this thesis deals with mixed species, multi-aged stands. Failure to adequately define mortality could lead to a who's on first, who's on second scenario (Abbot and Costello, 1939)

2.2.5.1 Regular Mortality

Within this thesis, the term regular mortality refers to the death of a tree captured by the expressed characteristics of the tree in conjunction with the characteristics of the

system in which the tree exists. Regular mortality is deterministic in nature (and is sometimes called deterministic mortality) and is exclusive of stochastic death, that is to say death can be foreseen or predicted.

Regular or deterministic (Oxford 1995) mortality is described as an inevitable consequence of an occurrence(s), cause(s) or event(s) that is the generating force for mortality. The current, or observed, state of a tree (alive or dead) is explainable, logically and rationally, by its known previous state and the actions on it within a discrete and definable system of which survival and death are components. It is possible to say that a tree is dead or alive within a system because of the antecedent state of the tree and the system. The terms regular mortality and deterministic mortality are then well applied to mortality resulting from competition or suppression because it suitably describes occurrences, events, or causes of mortality as being antecedents of the current, observable condition or state of a tree.

For practical purposes the observation of, and the ability to detect or observe mortality from a survey data set, are the primary considerations in modelling mortality from a system observed in such a manner. Expressed tree and stand characteristics combine to explain mortality due to competition or suppression for the resources necessary to sustain life. So the causal agent or agents of regular mortality are assumed to be competition or suppression.

2.2.5.2 Irregular Mortality

Irregular mortality, as applied in this thesis, is when the death of a tree is not captured by expressed tree characteristics. Irregular mortality occurs when the expressed characteristics of a tree and stand do not indicate death or impending death of

a tree and the tree is nevertheless, dead. Neither the tree nor the system of which it is a component provide any details as to the demise or impending demise of the tree; the death lacks antecedents. Since mortality of the tree is not due to suppression or competition, irregular mortality is regarded as stochastic. Irregular mortality of an individual tree is induced from a function of the system in which the tree is a component and is particular to the tree but not the system; this is the primary distinguishing feature from catastrophic mortality (section 2.2.5.6). That is to say the scale of the event, and the resulting mortality plays a role in defining irregular mortality. Events associated with irregular mortality include, for example: fire, windstorms, lightning, snow, ice, insect attacks and other herbivorous activity.

2.2.5.3 Regular and Irregular Mortality in an Empirical Data Set

Regular and irregular mortality are the two types of mortality examined within this thesis. There are limitations to detecting both types of mortality that must be considered. One of which is mingling of regular and irregular mortality in the data. If the causal agent or agents of irregular mortality acted upon a tree during an event near the end of a measurement interval, the expressed characteristics of a tree will be unable to indicate its demise. Likewise, if the causal agents of irregular mortality acted upon a tree during an event near the start of a measurement interval, the expressed characteristics of a tree will indicate that the tree died from causal agents of regular mortality. Furthermore, if the system indicates that conditions were suitable for survival then the death of a tree from irregular causes is confounded with trees that died from regular causes. A tree or system in which it exists may have characteristics that indicate a tree should be alive although the observed condition of the tree is dead. The reverse

condition is also true. This confounding of mortality detection and explanation is largely attributed to the presence of irregularly dead trees in the data.

Because time elapses between measurements such that a tree is alive at the first measurement and dead at the second measurement, and because the cause of death is unknown, there will be error present in the data set if all mortality is assumed to be regular. The expressed characteristics of a tree must be measured over a sufficiently short interval that the nature of the mortality is adequately characterized by the expressed characteristics. The longer the interval between measurements the greater will be the error of misclassification. If the measurement interval is too short the expressed characteristics will not change and if it is too long the expressed characteristics may be masked or worse confounded. Decline as a state of affairs for a tree is a prerequisite for modelling of regular mortality.

A basic distinction to be recognized is that regular mortality is predictable and irregular mortality is unpredictable. This is a problem in an empirical growth and yield data set because cause of death is not recorded and stochastic mortality is not clearly related to specific stand or site conditions (Jutras et al. 2003).

2.2.5.4 Stochastic Mortality

Stochastic (Oxford 1995) mortality includes a random component(s), as a feature of mortality within the system. The random component(s) exist(s) across both time and space. It includes chance or probability as a variable within the system. The occurrence(s), cause(s) or event(s) preceding the death of a tree are without antecedent, or at least in the situation of survey data, without observable antecedents.

2.2.5.5 Catastrophic Mortality

Catastrophic mortality is distinct from regular and irregular mortality in that the causal agents of death are not particular to a tree. The entire system under examination is affected and the causal agents render the system temporarily unsuitable for tree life. Agents responsible for catastrophic mortality include fires, mudslides, windthrow, snow, ice storms and/or insect attack.

An important distinction should be made to help separate and clarify irregular and catastrophic mortality because the causal agents (e.g., fire, mudslides, windthrow, insects, etc.) can be the same. The separating factors are intensity and extent of the actions and classification of actions or events as epidemic and endemic. In the case of irregular mortality intensity of causal agents is low within stands, affects only a portion of a stand, or a single tree, and is endemic or periodically endemic to a stand. For catastrophic mortality causal agents are intense, epidemic and affect entire stands.

2.3 STATISTICAL METHODS IN MORTALITY MODELLING

2.3.1 Introduction

The mathematical method chosen to model mortality in this thesis is logistic regression. Other methods such as artificial neural networks, simple and multiple linear regression are also available for modelling mortality. However, logistic regression is constrained to the interval [0, 1] and is therefore consistent with the objective of determining the binary state of trees of interest. In order for the reader to understand logistic regression and the methods associated with it, a brief review and explanation is presented.

2.3.2 Logistic Regression

The majority of individual-tree mortality models in the literature use logistic regression (e.g., Hamilton 1974, 1980 and 1986, Hamilton and Edwards 1976, Monserud 1976, Vanclay 1994, Eid and Tuhus 2001, Fridman and Stahl 2001, Hann and Hanus 2001, Bigler and Bugmann 2003, Hely et al. 2003, Jutras et al. 2003, Monserud and Sterba 1999, Yao et al. 2001, Alenius et al. 2003, Yang et al. 2003, Bigler et al. 2004).

Logistic regression is a form of nonlinear regression where outcomes are discrete, and error terms are not normally distributed (Chatterjee et al. 2000, Kutner et al. 2005). Circumstances exist in which a response, observation, choice or indicator of interest is present within a system in a dichotomous fashion. The binary response is considered nominal and represents data such as yes or no, up or down, and dead or alive. There is no magnitude or rank between responses and responses can be coded as 0 or 1 for no-response and response (i.e., alive or dead). Mortality as a response in an observational experiment involving repeated, discrete measures is dichotomous. In such cases a dichotomous, logistic regression model may be suitable for representing the phenomenon (Chatterjee et al. 2000, Kutner et al. 2005, StatSoft 2004).

The response predicted by the logistic model is a probability value that for discrete outcomes is coded as 0 or 1. For responses less than 0.5 a value of 0 is assigned as a response and for response values greater than or equal to 0.5 a value of 1 is assigned, although other cut-off values are also possible. This is useful when a discrete state is of interest. It can also be the case that the probability of mortality for a particular tree is the response of interest.

A logistic regression is preferred over a linear or non-linear regression in part because linear or non-linear regressions constrained to the response interval [0, 1] would

only be applicable to the data which gave rise to the model in the first place (Kutner et al. 2005). The logistic regression is optimal for binary data because it is sigmoidal (it has an S-shape), and approaches 0 and 1 asymptotically (the condition whereby the regression line approaches the curve limit arbitrarily closely (Weisstein 2004).

There are several problems that arise when a response variable is dichotomous. The first problem is that the error terms are not normally distributed (Kutner et al. 2005). This is obviously the case as error terms can only be one of two possible values (Kutner et al. 2005). Secondly, error variance is non-constant (Hamilton 1974, Kutner et al. 2005). Because of this, ordinary least squares is no longer optimal because error variance differs at different levels of X (the set of independent variables) (Kutner et al. 2005). Finally, the response function is constrained to being between 0 and 1 and is therefore not normally distributed (Kutner et al. 2005).

At this stage it is appropriate to introduce the symbol π which is used to denote the probability that $Y = 1$ when $X = x$ (Chatterjee et al. 2000). Since π is a probability it must lie between 0 and 1. It is also appropriate at this point to note that the normal distribution for the Y (dependent) observations is no longer used, instead the Bernoulli distribution for a binary random variable is used (Kutner et al. 2005). Since the distribution of error terms ε_i depends on the Bernoulli distribution of the response Yi, the multiple logistic regression is stated in the following fashion (Chatterjee et al. 2000, Kutner et al. 2005):

$$E(Y_i) = \pi_i = \frac{\exp(\beta_0 + \beta_1 X_1 + \beta_i X_i)}{1 + \exp(\beta_0 + \beta_1 X_1 + \beta_i X_i)} \quad (1)$$

where:
$E(Y_i)$ – is the Expected value of Y_i
Y_i – is the i^{th} observation
π_i – is the probability of the i^{th} observation
β_0 – is the constant for the model
β_1-β_i – are the coefficients for the X_i variable, and
X_1-X_i – represent variables of the model

In order to deal with problems associated with logistic regression special methods are required. Maximum likelihood methods are commonly used to parameterize variables in a logistic regression, and special model and variable testing procedures are used. Once the fitted logistic response function is obtained, the usual next steps are to examine appropriateness of fitted response functions and, if the fit is good, to make a variety of inferences and predictions (Kutner et al. 2005). Other parameterization methods such as the Quasi-Maximum Likelihood Method (discussed below) are also available. Models parameterized in such a fashion also require special tests for validation. As such, brief reviews of the Likelihood-Ratio and Wald Tests are presented along with short reviews of Deciles of Risk and Prediction Success Tables.

2.3.3 Maximum Likelihood Method

The maximum likelihood method is commonly used to estimate parameter values in logistic regression models and many individual-tree mortality models have been fitted using this method (e.g., Monserud and Sterba 1999, Hann and Hanus 2001, Yao et al. 2001, and Yang et al. 2003). Also, it is the method recommended by Vanclay (1994). Weighted and non-weighted nonlinear regressions are also been used (e.g., Hamilton and Edwards 1976, Buchmann et al. 1983) to estimate parameters, but the maximum

likelihood method is more commonly used because it is more straightforward than other methods (Monserud and Sterba 1999). Other methods of estimating parameter values for logistic regression equations include marginal quasi-likelihood and penalized quasi-likelihood (Alenius et al. 2003).

Maximum likelihood parameter estimates are those values of the parameter (β) that maximize the log-likelihood function of the model (Kutner et al. 2005). The reason that the maximum likelihood method is used to estimate parameters of logistic regression models, is because unknown parameters are non-linearly related to $\pi(x)$ (Alenius et al. 2003). Essentially, the method of maximum likelihood chooses as estimates those values of parameters most consistent with the sample data (Kutner et al. 2005).

The maximum likelihood method is well suited to dealing with problems associated with responses (Y_i) being binary (Kutner et al. 2005). It is known that when a response function is binary, assumptions of normality are no longer met. The Bernoulli distribution for a binary random variable is therefore used for the Y observations instead of the normal distribution (Kutner et al. 2005).

Model development was conducted using both Maximum Likelihood and Quasi-Maximum Likelihood although final model parameterization was completed using Quasi-Maximum Likelihood.

2.3.4 Quasi-Maximum Likelihood

In their work on evaluating estimation methods for logistic regression in modelling individual-tree mortality Alenius et al. (2003) investigated several methods of parameter estimation, including marginal quasi-likelihood and penalized quasi-

likelihood methods. They state that the maximum-likelihood and the marginal quasi-likelihood methods resulted in models with high sensitivity, a high-rate of correct classification and low bias. They also suggest that with relatively balanced data the marginal quasi-likelihood (MQL) method produces consistent model estimates for multilevel binary mortality models, and that logistic regression models with random effects, need special quasi-likelihood estimation methods.

When a model to be estimated by maximum likelihood is misspecified, standard errors and all hypothesis tests are unreliable (Steinberg and Colla 2005). This could be a serious problem since misspecification could be common rather than uncommon. The procedure of estimating a misspecified model is called the quasi-maximum likelihood (QML) estimation (Steinberg and Colla 2005). For a misspecified model, the likelihood-ratio test is not asymptotically chi-squared, and the Wald and Likelihood-Ratio tests are not asymptotically equivalent, even when the QML matrix is used for Wald tests (Steinberg and Colla 2005). Because of potential for misspecification and therefore incorrect interpretation of model results both the Likelihood-Ratio Test and the Wald Test are presented within this thesis. This approach permits the experimenter to make better decisions as regards model robustness.

2.3.5 Model and Variable Evaluation

A determination needs to be made when building a logistic regression model, such as the one in this thesis, as to which variables are worth keeping and which model is best, appropriate or suitable for the purpose of the modelling effort. Questions that are appropriate to ask include: "How well does this particular model fit the data" (Kutner et al. 2005, Steinberg and Colla 2005); and, "Are the results unduly influenced by a

handful of unusual observations" (Steinberg and Colla 2005)? In particular, for logistic regression models, it is necessary to examine the response function to see if it is monotonic and sigmoidal in shape (Kutner et al. 2005). To answer these questions, model assessment tools as provided by a software package such as DataDesk 6 and/or Systat 11 are used. The tools available include: prediction success table, log-likelihood, likelihood-ratio tests, McFadden's Rho-Squared, odds ratios, Chi-square and Hosmer-Lemeshow statistics, as well as graphical analysis of residuals. Caution must be exercised when using goodness-of-fit tests since they are usually not sensitive when the fit is poor for just a few cases (Kutner et al. 2005).

A brief review of coefficients, likelihood, Likelihood Ratio Test, Wald Test, McFadden's Rho-Squared, Odds Ratio, Deciles of Risk, Hosmer-Lemeshow Goodness-of-Fit Statistic and the Prediction Success Table is presented so that the reader will understand each feature and the function it performs in evaluating the model developed in this thesis.

2.3.5.1 Coefficients

Coefficients in a logistic regression model are evaluated similar to those in a linear regression (Steinberg and Colla 2005). When a coefficient of a variable is large relative to its standard error (t-ratio) then the variable potentially is an important predictor (Steinberg and Colla 2005), however, interpretation of a coefficient in logistic regression is different from ordinary regression. In logistic regression the coefficient tells how much the logit increases for a unit increase in the independent variable, but the probability of a 0 or 1 outcome is a nonlinear function of the logit (Steinberg and Colla 2005).

2.3.5.2 Likelihood

One measure of model fit to a set of data is the likelihood (Bergerud 1996). A likelihood is the hypothetical probability that an event that has already occurred would yield a specific outcome; it refers to past events with known outcomes (Kutner et al. 2005). The likelihood is estimated using the method of maximum likelihood, which chooses as estimates those values of the parameters most consistent with the sample data (Kutner et al. 2005). For discrete data, the maximum likelihood method is derived from a probability function, such as the binomial distribution, that predicts probability of obtaining specific data values given known values of parameters (Bergerud 1996).

Each logistic regression model, fitted to the same set of data, has a corresponding log-likelihood value calculated at the maximum likelihood estimates for that model. If a second model, in the form of a submodel, is fit to the same set of data, the log-likelihoods (LL) of the two models can be assessed relative to each other. The greater the likelihood, the better the fit (StatSoft 2004). The difference between the two models can be assessed for significance using the likelihood-ratio test. In general, suppose that model 1 has t parameters, while model 2 is a subset of model 1 with only r of the t parameters so that $r < t$. Model 1 will have a higher log-likelihood than model 2 (a submodel of a larger model will always have a smaller likelihood, so the models must be assessed using a test). For large sample sizes, the difference between these two likelihoods, multiplied by two, will behave like the chi-square distribution with t-r degrees of freedom. This can be used to test the null hypothesis that the t-r (t minus r) parameters not in both models are collectively equal to zero (Bergerud 1996), that is, they have no effect on results.

2.3.5.3 Likelihood-Ratio Test

The two types of hypothesis test for the logistic regression model are the likelihood-ratio (LR) test and the Wald test (Steinberg and Colla 2005). The properties of the two tests are based on asymptotic theory and will yield identical results when sample size is very large (Steinberg and Colla 2005). Both tests attempt to determine if all coefficients in the model except the constant are equal to zero (Chatterjee et al. 2000, Steinberg and Colla 2005). If the null hypothesis is rejected in favour of the alternative hypothesis then the model has some explanatory power.

When constructing a model, it may be of interest to determine whether a subset of the X variables in a multiple logistic regression model can be dropped; i.e., testing whether associated regression coefficients equal zero (Kutner et al. 2005, Steinberg and Colla 2005). The likelihood-ratio test is conducted by fitting two nested models (the restricted and the unrestricted) and comparing the log-likelihood at convergence (Steinberg and Colla 2005). Typically, the unrestricted model contains a proposed set of variables, and the restricted model omits a selected subset, although other restrictions are possible (Steinberg and Colla 2005).

The Likelihood-ratio test is: [2*(LL(N)-LL(O))], (where: LL is log-likelihood, N is the model of interest, and O is the null model). The test has degrees of freedom equal to the number of covariates in the model, not including the constant (Chatterjee et al. 2000, StatSoft 2004, Steinberg and Colla 2005). Models can also be assessed relative to one another in an effort to determine which variables should be retained. The p-value for the likelihood-ratio test indicates that the null hypothesis will be rejected if it is less than the accepted cut off (Steinberg and Colla 2005).

2.3.5.4 The Wald Test

A test of whether a single parameter is zero is conducted as a Wald test by dividing the squared coefficient by its variance and referring the result to a chi-squared distribution with one degree of freedom. Each t-ratio is the square root of a simple Wald test (Steinberg and Colla 2005).

The Wald Test, tests a specific parameter in a model. The null hypothesis of the test is that the parameter in question is zero, while the alternative hypothesis is that the parameter in question is not zero. The test is conducted by squaring the t-value (the ratio of the parameter estimate divided by its estimated standard error) and outputting it as a chi-square value and referring it to a chi-squared distribution with one degree of freedom (Steinberg and Colla 2005). If the associated p-value is less than 0.05 then the null hypothesis is rejected in favour of the alternative hypothesis and the parameter is deemed to have some value to the model.

Wald tests are helpful for deciding if a variable or term in a model should be dropped (Bergerud 1996). The decision to drop or retain a variable is specific to the regression equation in question. A variable might or might not be useful in another formulation of the logistic regression model. The Wald test is considered a "last-in" test; it tests whether the current term, if it was the last term added to the model, substantially reduces the log-likelihood (Bergerud 1996). Wald statistics are considered approximate and somewhat unreliable (Bergerud 1996), so marginally significant results should be confirmed by fitting models with and without the terms of interest, and then conducting the corresponding deviance test (Bergerud 1996).

2.3.5.5 The Wald Test versus the Likelihood-Ratio Test

Steinberg and Colla (2005) state that the two tests will give identical results as the sample size nears infinity. Steinberg and Colla (2005) give three reasons for choosing the Likelihood-Ratio test over the Wald test:

1. The likelihood is the fundamental measure on which model fitting is based;
2. Monte Carlo studies suggest that the likelihood-ratio statistic is more reliable with small samples; and
3. A nonlinear constraint can be imposed on the parameter estimates and simply tested by estimating restricted and unrestricted models.

Since there is some doubt as to the reliability of the Likelihood-Ratio test when QML methods are used for parameter estimation and because the Wald Test may be unreliable, the results of both tests are presented.

2.3.5.6 McFadden's Rho-Squared

McFadden's Rho-squared is a transformation of the likelihood-ratio statistic intended to mimic an R-squared value (Steinberg and Colla 2005). It is a measure of the variance, and should not be interpreted as a goodness-of-fit statistic. It is always between 0 and 1, and a higher Rho-squared corresponds to a lower variance (Steinberg and Colla 2005). Rho-squared tends to be much lower than R-squared though, and a low number does not necessarily imply a poor fit. Values between 0.20 and 0.40 are considered very satisfactory (Hensher and Johnson 1981). McFadden's Rho-Squared results for the final model and the tested sub-models are presented in tabular format in the Results section.

2.3.5.7 Odds Ratio

The odds ratio is the multiplicative factor by which the odds change when the independent variable increases by one unit while the others are held constant (Chatterjee et al. 2000, Steinberg and Colla 2005). The odds of the response are given by $\pi/(1-\pi)$, where π is the probability of response and $1-\pi$ is the reference (Chatterjee et al. 2000, Steinberg and Colla 2005). If the confidence interval for the odds ratio does not contain the value 1 then the variable in question significantly affects the odds ratio (Chatterjee et al. 2000, Steinberg and Colla 2005). If the interval is below 1 the variable lowers significantly the relative odds, while if the interval lies above 1 then the relative odds is significantly increased by the variable (Chatterjee et al. 2000, Steinberg and Colla 2005). A table of Odds Ratios for the fitted model and sub-models used in testing the final model are presented in the Results section.

2.3.5.8 Deciles of Risk

Deciles of risk help to ensure that the model fits the data and that the results are not unduly influenced by a handful of unusual observations (Steinberg and Colla 2005). The goodness-of-fit statistic associated with the deciles of risk will depend on the grouping rule specified (Steinberg and Colla 2005). Methods available in Systat to help ensure that the model fits the data include goodness-of-fit statistics, and a collection of residual, leverage and influence quantities (Steinberg and Colla 2005).

2.3.5.9 Hosmer-Lemeshow Goodness of Fit

Many of the logistic regression mortality models developed and presented in the literature have used the Hosmer-Lemeshow goodness-of-fit statistic to select final models and examine model fit (e.g. Yao et al. 2001, Yang et al. 2003). The Hosmer-

Lemeshow goodness-of-fit test is useful for unreplicated data sets or for data sets containing just a few replicated observations (StatsDirect 2004, Kutner et al. 2005).

Caution should be employed when using the ordinary Hosmer-Lemeshow test because it may not be reliable since it assumes independence among observations (Alenius et al. 2003). Observations in a growth and yield data set are not independent since there is more than one tree in each stand and plot, and there may also be a lack of independence between plots (Alenius et al. 2003). Yao et al. (2001) stated that since data for their study included multiple measurements for the same trees, observations were not independent, and a serial correlation existed among the data. When a tree is measured twice at two different points in time the second measurement is dependent on the first. As such, the data are not independently distributed and, therefore, violate the assumption of independence among error terms. Growth and yield data sets have a high degree of correlation among trees within the same plot and possibly between plots as well. As such, the use of the Hosmer-Lemeshow test for growth and yield data sets is suspect.

Alenius et al. (2003) point out that a basic problem with goodness-of-fit measures in the case of multi-level logistic regression is that all tests based on likelihood are approximations, because the likelihood is also an approximation. Caution must therefore be used when testing a model using the Hosmer-Lemeshow goodness-of-fit test. When examining model fit it is important to remember that prediction may be as important if not more important than a high numerical value of model fitness. A selection of predictions based on the selected model and several additional models is presented.

2.3.5.10 Prediction Success Table

When generating a logistic regression, Systat produces a prediction success table. The interpretation of the table proceeds as follows (Steinberg and Colla 2005):

> "The correct row is the proportion of records that were successfully predicted according to the estimated model. Correct is also known as sensitivity for the response group and specificity for the reference group. The false reference rate is the proportion of those predicted to respond that did not and the false response rate is the proportion of those predicted to not respond that actually did respond. The total correct is the proportion of correctly predicted references and responses. Success Index is the gain that the model shows over a purely random model that assigned the same probability to the dependent variable to every observation in the model."

The prediction success table is very useful for examining model functioning and is used to examine behaviour of a multitude of predictor variables. When the number of variables in question is reduced to a manageable size, variables can be entered or removed from the model singly or in combinations to assess their effect of on the model. Various Prediction Success Tables are presented to allow a more thorough evaluation of the final model.

2.3.5.11 Correlation

Yang et al. (2003) point out that from the statistical perspective, some predictor variables are correlated with each other, and, when this occurs, a change in one variable will lead to a change in correlated variables. In their logistic regression mortality model they do not give a quantitative interpretation of estimated coefficients due to presence of multicollinearity within the model.

Borders et al. (1987) found that for permanent sample plot data with more than three measurements, temporal correlation did not occur for non-overlapping growth intervals. Gertner (1987) noted that as measurement interval length increased, temporal

correlation decreased. In the literature, the problem of spatial correlation has generally been dealt with by ignoring correlation and assuming that each tree is an independent observation. Hamilton and Edwards (1976) in fitting their model assume that each tree is an independent observation and ignore the fact that there is some clustering in the selection of sample trees. This is similar to Yao et al. (2001) who state that, since they were developing a distance-independent mortality model, spatial correlation among trees was not considered and observations were assumed to be spatially independent even though there is likely spatial dependence. Yang et al. (2003) argue that since there are fewer mortality trees within each plot, within-plot spatial correlation should be trivial.

2.3.6 Data Splitting and Model Validation

Data splitting was considered in this thesis for model validation. However, as a means of validating the model, data splitting was not used. One reason was that there was only a small amount of data available, and removing some data for testing at a later time had the potential to make model development difficult. Another reason was that it has been indicated in the literature that it may not be appropriate to test forest models with split data.

The practice of splitting the data set into two portions and using one for development of a model and the other for a so-called independent test data set is questionable. "The split data sets are not independent of each other, as a result the data-splitting scheme used in model validation is not validating a fitted model but rather the sampling technique used to partition the data (Huang et al. 2003)." A decision, therefore, was made to use an independent data set to examine the model.

Model performance can be evaluated by considering how well a model fits the development data, how well the model fits an independent data set, and how well the models fits biological reality (Hamilton 1986). Because quality of fit does not necessarily reflect quality of prediction, an assessment of a model's validity on a separate data set is needed (Huang et al. 2003). In practice, if there is no other data set available for testing, splitting the data set into two groups may be the only means available for testing the predictive ability of a model.

2.3.7 Methodological Summary

The above statistical review provides an understanding of material presented in both the Methods and Materials, and Results Sections. It is also intended to act as a platform for a common understanding of the Methods. Logistic regression models are common for mortality modelling but are not common in other areas of forest modelling. As such, a cogency of the topic cannot be assumed and it is hoped that the Methodology Review has to some extent corrected that problem.

3 METHODS AND MATERIALS

3.1 MATERIALS

Two data sets were used in this thesis. The first data set, used for model development, was the AmericanCan data set (ACDS), also referred to in the thesis as the developmental data set. The second data set, used as an independent data set for model validation, was the Kimberly Clark data set (KCDS). It is also referred to as the alternative data set or the independent data set.

Both data sets commenced in the early 1950's and have continued through to the present time for the ACDS and to the 1990's for the KCDS. There are some interruptions in both data sets. The ACDS for instance, has few or no observations in the 1980's with the exception of 1980. It is also inconsistent with respect to time intervals between plot measurement. The re-measurement interval should be five-years for all plots, however, intervals are 4, 5, 6, 8, and 10 years. Some plots appear to have been measured early and others late. Within this thesis only data observations with a five-year measurement interval were used and model prediction results are valid for such intervals.

The AmericanCan and Kimberly Clark data sets respectively contain over 170,000 and 78,000 data records each. A total of 814 observations were available from the ACDS for model construction. Some plots and trees in the data sets had seven measurements. The ACDS had no height information available for the period of

interest. Height information only became available after the 1980's. Since there were too few observations available for that period that time interval and subsequently height were not used. Information that was available included tree diameter (cm), plot size (ha), tree number, plot number, and year of measurement.

Detection of understory ingrowth was determined with the use of record tagging and queries. Each plot and each tree was given a measurement number starting with the first time the plot or tree was recorded in the data set. By examining the two numbers it was possible to determine if a given tree was ingrowth or not. It was also possible to determine if a tree was ingrowth by examining tree size in relation to all trees in a plot and all trees of the same species in a plot. To be classified as ingrowth, a tree was required to grow into the plot by height increment and not grow into the plot by diameter increment. This simply means that if the corner to corner plot boundary was broken by virtue of a tree increasing in diameter it was not considered as an understory ingrowth observation.

The KCDS is similar to the ACDS, however, fewer suitable records were available from the KCDS. It was, nevertheless, deemed suitable as an alternative data set. Several modifications were necessary prior to its use and the modifications include using a modified ingrowth density variable and modified ingrowth variable. These are described in the Results and Discussion section.

The plots for both data sets are in North Central Ontario in the Longlac area. The areas, which are covered by the data sets, do not overlap geographically. The plots for the ACDS plots are of three size 0.04 ha, 0.08 ha and 0.12 ha, while the KCDS plots are either 0.04 ha or 0.08 ha. Because of how the data were chosen, no 0.12 ha plots

were included in the developmental data. That it to say, the exclusion of the 0.12 ha plots was not deliberate, rather it was a result of the process of data selection.

To be classified as mixed species each plot was required to have at least two species. Although there was a lack of site information in the data set itself it is known that ACDS plots were generally established on sites with better than average conditions (Penner 2003). For more information on the two data sets, see Popadiouk et al. (2003). Both data sets were provided courtesy of the Ontario Ministry of Natural Resources.

3.2 MODEL DEVELOPMENT

For the purposes of this thesis, a model in the form of a logistic regression equation was constructed using quasi-maximum likelihood methods. It was tested using Likelihood-Ratio and Wald Tests. The fit was determined to be acceptable with the use of three goodness-of-fit statistics (Hosmer-Lemeshow, Pearson and Deviance). The residuals were examined graphically for outliers and model adequacy. Finally, the proposed model was analyzed using an independent data set.

Seven variables were developed from two primary pieces of information: (1) diameter at breast height (dbh) and (2) instance of existence. Variables used in the model, as well as those considered and rejected, were primarily calculated from those two pieces of information. Plot size, plot identification number, measurement period, measurement interval, year of measurement, tree identification number and tree species were also available and were used to further develop and calculate variables. Plot size was used to calculate stand basal area in conjunction with diameter at breast height of each tree. Plot identification number and tree identification number were used to

separate trees and plots. Year of measurement and tree identification number were used to determine survival and mortality status for each measurement period. Plot and tree identification number and year of measurement were also used to determine plot density (stem count). Plot density was then converted to an estimate of stems per hectare in conjunction with plot size.

There was some additional information available, however, it was not used largely because it was not applicable within the constraints of the analysis. For example, there was some height information available but only for the plots measured in the 1990's and later. Since, only plots between 1950 and 1981 were used, height information was not applicable. A similar problem existed for site index. The additional information available but not used included: stand age (stand establishment year), site index species, vegetation type, soil type, ecosite, latitude, longitude and some soils information.

The proposed seven-variable model was tested using the Likelihood-Ratio and Wald Tests. For the Likelihood-Ratio Test this included testing against the null model and then against each of the seven possible six-variable models. Each six-variable model consisted of the seven-variable model with a different variable dropped each time the test was run.

The Likelihood-Ratio and Wald Tests indicated that a single variable, diameter at breast height squared, was insignificant. It was therefore dropped. The new six-variable model was then estimated and the same Likelihood-Ratio and Wald Tests as above were conducted. Neither the Likelihood-Ratio Tests nor the Wald Tests rejected any of the remaining six variables nor the model itself. Finally, a prediction success table, odds ratios, and goodness-of-fit statistics were calculated for the six-variable model.

3.3 FINAL MODEL SELECTION

As already indicated, many variables were, or could be, calculated or derived from the available information, but development of the final model was done using seven variables. The seven-variables are discussed below and presented in Table 1.

The variable TROOT is used to detect mortality of trees with low relative vigour. To obtain a measure of a tree's vigour for its size, its diameter at breast height (cm) is multiplied by its change in diameter at breast height (vigour). Further incorporating stand basal area (m^2/ha) into the variable allowed relative performance of a tree in relation to the stand in which it existed to be assessed. Because each plot was expected to have a different growing capacity (site quality), developmental stage, composition, stage of crown closure, and so on, it was important to minimize bias between sites by standardizing performance of a tree within its specific environment by using basal area.

The purpose of the TREE variable was to relate specific size of an individual understory ingrowth black spruce tree to other understory ingrowth black spruce trees in a stand. Understory individuals may commence shortly after stand initiation or at a later stand developmental stage. Regardless of the temporal point of initiation of any particular individual, all understory ingrowth black spruce individuals share a common trait, that is, they occupy a sub-canopy position in a stand. Because of this, size of each individual in relation to the size of other trees in a similar situation is important, because it is a relative assessment of a tree and of the stand in which it occurs. Several hypotheses have been made in the literature as regards tree size and its relationship to mortality. Waring (1987) has indicated that larger trees may by more susceptible to stress because of greater demands for water, respiration, and photosynthate.

Table 1. Variables used in final model development.

Variable Acronym	Variable ID	Variable Description*
TROOT	V1	$\sqrt[3]{\frac{dbh * din}{ba}}$ Third root of – dbh multiplied by diameter increment – and divided by stand basal area. Variable is intended to capture the size and vigour of the tree within the stand.
TREE	V2	$\frac{dbh}{avsbingdbh}$ Individual tree dbh divided by average dbh of ingrowth black spruce for stand (*avsbingdbh*). Variable relates a particular tree to all the other understory ingrowth black spruce in the plot.
SQD2BA	V3	$\sqrt{\frac{dbh^2}{ba}}$ The square root of – individual tree dbh squared divided by basal area stand. Hypothesized to capture mortality of larger understory ingrowth individuals.
DENBA	V4	$\left(\frac{IngrowthDensity}{BasalArea}\right) * \left(\frac{OverstoryDensity}{BasalArea}\right)$ Density of ingrowth divided by basal area of the stand, multiplied by density of overstory divided by stand basal area. A proxy measure of competition.
DBHSQRD	V5	dbh^2 Square of individual tree dbh. Variable proposed as being useful for detecting mortality of large trees.
D2BA	V6	$\frac{dbh^2}{ba}$ A modification of dbh^2 incorporating stand basal area.
AVDBH	V7	$\sum_{i=1}^{n} \frac{dbh}{n}$ Average dbh of all trees in the plot.

*dbh – diameter at breast height (cm), din – diameter increment measured at dbh (cm) for the 5-year period, ba – basal area (m^2/ha), Ingrowth Density –stem count of understory ingrowth individuals for the plot converted to a per ha value, Overstory Density – stem count of individuals in the plot that were not understory ingrowth individuals, converted to a per ha value, n – the number of trees observed within the plot.

This is also likely the case for understory individuals. However, a larger understory individual may be better able to respond to a release opportunity than a smaller

individual because of it physical properties (i.e. crown size and root capacity). So a smaller tree may have a higher survival probability under a dense canopy but be less favourably positioned to respond to a growth opportunity. Because of this, a tree in the understory must only be as big as necessary to survive in the understory. For smaller trees in an understory position it may be the case that they simply cannot acquire enough of the necessities of life to enable survival.

SQD2BA and D2BA are similar variables, differentiated by a simple square root transformation. In both cases the variables are intended to emphasize susceptibility of larger trees within their environment. A larger tree in a stand with a high basal area may face strong competition for light, nutrients, water and physical growing space, whereas a tree of the same size in a stand with a low (or lower) basal area faces reduced pressure for the same life sustaining variables. The intended effect of squaring the size of individual trees is to emphasize susceptibility of larger trees to competitive pressures. Standardizing the square of tree size with basal area allows competitive stress (stresses) induced by a stand upon a tree to be related to tree size. Since a stand with a lower basal area can be expected to have a reduced level of competitive stresses, basal area is a good means of incorporating stand pressures.

Both SQD2BA and D2BA are included in the model because they emphasize different tree patterns. As will be shown later, neither variable can be omitted without degrading the model.

AVDBH is intended to represent average diameter at breast height of all trees on a site, inclusive of stand density and basal area. A site may have trees with large or small diameters, but dense stands will have lower average tree diameters.

A very basic problem with measuring total quantity of trees on a boreal mixed species site is the interaction between summation of the instance of existence for individual trees and summed planar area of all individuals considered at a standard height. An understory with a large number of individuals will not contribute significantly to total basal area. Both basal area and density fail to adequately convey stand conditions. They also both fail to convey a relationship between tree size and total number of trees present. Density may be high while basal area is low and vice versa. Additionally, neither measure considers structural complexity of a stand, nor that different species do not contribute evenly (*vis a vis* stem diameter and crown diameter/length). In an attempt to partially rectify this problem, overstory and understory densities (stem counts per ha) are both divided by stand basal area to give stand level estimates of structural complexity, and tree size, for each stand structural component. The result was DENBA. The division of density by basal area assigns each observed individual a portion of the planar area of the stand. The two are then multiplied together so that the difference between understory and overstory can be approximated as a single value. By accounting for two different structural components of the stand a better relationship between the understory and the overstory is developed.

DBHSQRD is a prevalent variable in the literature and is used to predict mortality of larger individuals. Because the square of size of individuals within a population is more emphatic of larger individuals (e.g., a non-linear increasing curve), the square of size should allow a model to differentiate mortality for large individuals from small individuals. Since this is a possibility with the understory of complex stands as well as for the overstory, and as well as for simple stands, it is potentially a significant variable.

Likelihood-Ratio and Wald Tests were used to determine which, if any, of the final variables in the model were extraneous.

3.5 RESIDUAL ANALYSIS

Residuals of the selected model were examined graphically to determine if there were any influential outliers and to see if the model was adequate. Methods for detecting influential outliers in logistic regression are limited. Four types of residuals were calculated: Ordinary residuals, Pearson residuals, Studentized Pearson residuals and Deviance residuals.

The four types of residuals were plotted against estimated probabilities of the observations. Each type of residual was plotted against the estimated probability and a Lowess Smooth line was added. The purpose of a Lowess Smooth line in an examination of residuals of a logistic regression model is to detect model inadequacy. If the line is approximately horizontal with zero intercept then the model is adequate. It is recognized that this is only one measure of model adequacy.

Next, changes in Pearson Chi-Square values were plotted against estimated probabilities. Outliers appear as high scores and are located high on the y-axis in comparison to the rest of the data. Those data points thought to be outliers were eliminated and the model was re-estimated. In a similar technique the change in the deviance residuals were plotted against the estimated probabilities. The detection of outliers was similar and data points that were, potentially, outliers were eliminated in an iterative fashion starting with the highest score.

As a last examination of the residuals, a graph of Hadi's Influence Index was plotted against Studentized Pearson Residuals. Hadi's Influence Index shows both potential of a point to influence the regression (related to its leverage) and the studentized residual, which indicates whether a point exercises its potential (Velleman 1988). Points found near either axis are not influential, while those found in the upper right quadrant of the display are considered to be strongly influential.

As a last step in graphically analysing the model, two final graphs were produced and are presented in the Results section. The first was of the estimated probabilities plotted against the expected value for a normal distribution, and the second was of the estimated probabilities plotted against the linear predictors.

3.6 MODEL USE WITH AN INDEPENDENT DATA SET

The next and final step in model testing was to use the model with an independent data set. Predictions of survival or mortality were made using the developed model and the independent data. The desired outcome was to demonstrate that the model is in fact robust and is capable of accurately predicting mortality of understory ingrowth black spruce individuals in boreal mixed species stands.

4 RESULTS AND DISCUSSION

4.1 FINAL MODEL SELECTION

Table 2 contains p-values for each variable included in the seven-variable model, and each of the seven possible six-variable models. As a preliminary means of investigating performance of a variable within a model, the p-value is used to assess variable significance. Variable p-values of the seven-variable model indicate that DBHSQRD is potentially insignificant, however, it must be recognized that addition or subtraction of a variable has potential to affect the entire model, so each revised model must be considered separately.

Table 3, which lists score values for the Likelihood-Ratio and Wald Tests, indicates that the seven-variable model and each six-variable model are significantly different from a null model (a model with only a constant). This means that each model has some explanatory power. Both the Likelihood-Ratio Test (p=0.1571) and the Wald Test (p=0.1839) in Table 3 show that DBHSQRD is insignificant. Both test scores have p-values much greater than 0.05, indicating that the variable is insignificant.

Each of the seven possible six-variable models is compared to the seven-variable model under the null hypothesis that the six-variable model in question is not significantly different from the seven-variable model. For either the Likelihood-Ratio Test or the Wald Test if the reported p-value is greater than 0.05 then the variable is potentially insignificant.

Table 2. Coefficient p-values for seven-variable and six-variable models.

	CONSTANT	TROOT	TREE	SQD2BA	DENBA	DBHSQRD	D2BA	AVDBH
7 VM	≤0.0001	≤0.0001	0.0016	≤0.0001	≤0.0001	0.1839	0.0102	0.0110
6 VM (TROOT)*	≤0.0001	---	0.0065	≤0.0001	≤0.0001	0.2165	0.0000	0.0083
6 VM (TREE)	≤0.0001	≤0.0001	---	0.0001	≤0.0001	0.0005	0.2994	≤0.0001
6 VM (SQD2BA)	0.0307	≤0.0001	0.0572	---	≤0.0001	0.0806	0.0433	0.0037
6 VM (DENBA)	0.0139	≤0.0001	≤0.0001	≤0.0001	---	0.2516	0.3621	0.6959
6 VM (DBHSQRD)	≤0.0001	≤0.0001	≤0.0001	≤0.0001	≤0.0001	---	≤0.0001	0.0144
6 VM (D2BA)	0.0002	≤0.0001	0.0041	0.0001	≤0.0001	0.0047	---	0.0058
6 VM (AVDBH)	0.0001	≤0.0001	≤0.0001	≤0.0001	≤0.0001	0.7388	0.0001	---

*The variable in brackets has been removed as a variable of the model.

Table 3. Likelihood-Ratio and Wald Test scores for seven-variable and six-variable models.

	7 VM	6 VM* (TROOT)	6 VM (TREE)	6 VM (SQD2BA)	6 VM (DENBA)	6 VM (DBHSQRD)	6 VM (D2BA)	6 VM (AVDBH)
LL(N)	-361.9746	-372.3811	-368.5518	-370.2289	-378.8681	-362.9747	-363.2740	-366.2965
LL(O)	-469.9469	-469.9469	-469.9469	-469.9469	-469.9469	-469.9469	-469.9469	-469.9469
LR Test (Null)	215.9446	195.1316	202.7901	199.4358	182.1574	213.9444	213.3456	207.3007
LR Test p-value	≤0.0001	≤0.0001	≤0.0001	≤0.0001	≤0.0001	≤0.0001	≤0.0001	≤0.0001
LR (6v7)	---	20.8130	13.1545	16.5088	33.7871	2.0002	2.5990	8.6439
LR (6v7) p-value	---	≤0.0001	0.0003	≤0.0001	≤0.0001	0.1571	0.1069	0.0033
Wald	---	18.1699	9.9459	22.2554	22.0739	1.7660	6.5955	6.4731
Wald p-value	---	≤0.0001	0.0016	≤0.0001	≤0.0001	0.1839	0.0102	0.0110
Rho-Squared**	0.2298	0.2076	0.2158	0.2122	0.1938	0.2276	0.2270	0.2206
Correct Response	0.4479	0.4282	0.4352	0.4337	0.4294	0.4469	0.4456	0.4440
Correct Reference	0.8018	0.7948	0.7973	0.7968	0.7952	0.8015	0.8010	0.8004
Total Correct	0.7083	0.6979	0.7016	0.7009	0.6986	0.7078	0.7071	0.7063

*The variable in brackets has been removed as a variable of the model.

**McFadden's Rho-Squared

The Likelihood-Ratio Test rejects two of the six-variable models (6 VM (DBHSQRD) and 6 VM (D2BA)), while the Wald Test rejects one of the six-variable models (6 VM (DBHSQRD)). For the tested models and variables the removal of any one of the variables TROOT, TREE, SQD2BA, DENBA or AVDBH affects the model significantly. The Likelihood-Ratio test thus indicates that the variables DBHSQRD and D2BA can be removed from the model without significantly affecting the model's performance. The Wald Test does not reject the model with D2BA removed so further investigation is required. Also important to consider is that two variables should not be removed from contention simultaneously because each model is unique.

When DBHSQRD is removed as a variable of the model, the resultant six-variable model has all significant variable p-values as can be seen in the table row marked 6 VM (DBHSQRD) in Table 2. The Likelihood-Ratio and Wald Test scores for the six-variable model with DBHSQRD missing (Table 3) indicate that the model is not significantly different from the seven-variable model and as such DBHSQRD has no significant affect in the model.

This is a significant find because it may indicate that tree size does not have the same implications for understory trees as it does for overstory trees. Although tree size may still be an important predictor of mortality, larger understory ingrowth are not significantly more susceptible to mortality than smaller understory ingrowth, or at least not detectably so.

An additional observation about Table 2 is that both D2BA and AVDBH have p-values that fluctuate between significant and insignificant. Although, in the six-variable model where DBHSQRD is removed as a variable, both D2BA and AVDBH are significant variables. Referring again to the results of the Likelihood-Ratio and Wald

Test scores (Table 3), it can be seen that the Likelihood-Ratio Test indicates no significant difference for the model when eliminating D2BA, while the Wald Test indicates that the elimination of D2BA produces significantly different results. Both the Likelihood-Ratio Test and the Wald Test indicate that the removal of AVDBH produces a model that is significantly different from the seven-variable model. For all other models, the Likelihood-Ratio Test and the Wald Test indicate that removal of the variable has a significant effect.

For the model where AVDBH is removed and DBHSQRD remains as a component of the model, it is noticeable that the p-value for DBHSQRD is large. A model was built with AVDBH and DBHSQRD as an interaction term (not presented here). The purpose of which was to see if the interaction between the two variables was significant. The p-values indicated that the interaction term was insignificant.

Consistent performers across the six-variable models were TROOT, TREE, SQD2BA and DENBA. There is some doubt cast as to the significance of the variables DBHSQRD, D2BA and AVDBH. Other mortality modelling efforts have made use of DBHSQRD as a variable to predict mortality of larger individuals. The analysis has shown that the variable DBHSQRD appears to be a poor performer in general. A potential reason for this is that the system being examined is understory ingrowth and not whole stands. The value of the variable is limited because the potential relationship between size and mortality has changed.

Based on the Wald Test and Likelihood-Ratio Test results, the variable DBHSQRD was dropped from further testing. The resulting six-variable model was then tested against each of the six possible five-variable models.

The variable p-values for the six-variable model are presented in Table 4 along with the variable p-values for each possible five-variable model. The variable p-values remain significant with two-exceptions. In the first case, where SQD2BA is removed, both the constant and D2BA become insignificant variables. In the second case where DENBA is removed, AVDBH becomes an insignificant variable. This is the same effect that was seen when the six-variable models were being tested. A closer examination of the models using the Likelihood-Ratio and Wald Tests is required (Table 5).

One important piece of information displayed by Table 4 is that all of the variables for the six-variable model have significant p-values. This is a first indication of a potentially significant model. Likelihood-Ratio Test scores for the six-variable model against the null model and each possible five-variable model against the six-variable model are displayed in Table 5. The Wald Test Scores for each five-variable model also indicate a rejection of the null hypothesis. According to both the Likelihood-Ratio Test and the Wald Test the omission of any one of the six remaining variables results in a model that performs significantly poorer than the six-variable model. This includes the five-variable models with D2BA and AVDBH removed.

It is important to note that the McFadden's Rho-Squared value for the D2BA omitted model and the AVDBH omitted models, are the two highest scores of the six five-variable models presented. This does not mean that these two models provided better predictions but it does indicate that the fit of the curve to the data is superior when those two variables are included as variables. McFadden's Rho-Squared for the six-variable model is the largest score indicating a better fit than any of the five-variable models.

Since the six-variable model has significant variables (according to the p-values) and because the Likelihood-Ratio and Wald Tests indicate that eliminating a variable results in a degradation of the model, the six-variable model is selected as being acceptable. The model in the form already described (logistic) is presented in Table 6. The estimated coefficients for the selected model are presented in Table 7. Table 8 is the prediction success table for the selected six-variable model. The model has a correct prediction rate of 45%, a correct response rate of 80% and a total correct prediction rate of 70%. The false reference rate (incorrectly classified as dead by the model) is 55.3% and the false response rate (incorrectly classified as alive by the model) is 20%. Success Index, as previously discussed, is the gain of the selected model over a purely random model (one in which the same probability of response is assigned to every observation). The selected model, as such, has an 18% gain for selecting mortality and a 6% gain for predicting survival. Although Table 8 lists prediction success, it does so using data from which the model was developed. While this is adequate for an initial examination of the model and is in itself informative, a similar prediction effort is necessary with an independent data set for an independent verification of the model.

As will be seen in section 4.3 many probabilities generated by the model are in the middle range (e.g., 0.40 to 0.60). This is an indication that the model was unable to differentiate status of a particular observation as being dead or alive. In future modelling efforts it may be appropriate to have a lower and an upper cut-off such that ambiguous trees and predictions are not included as components of the prediction success table. It may also be appropriate to further investigate those trees which have ambiguous probability values.

Table 4. Coefficient p-values for six-variable and five-variable models.

	CONSTANT	TROOT	TREE	SQD2BA	DENBA	D2BA	AVDBH
6 VM	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0144
5 VM (TROOT)	0.0000	---	0.0002	0.0000	0.0000	0.0000	0.0108
5 VM (TREE)	0.0000	0.0001	---	0.0013	0.0000	0.0006	0.0001
5 VM (SQD2BA)	0.0598	0.0000	0.0088	---	0.0000	0.1297	0.0060
5 VM (DENBA)	0.0024	0.0000	0.0000	0.0000	---	0.0000	0.0980
5 VM (D2BA)	0.0023	0.0000	0.0003	0.0021	0.0000	---	0.0164
5 VM (AVDBH)	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	---

Table 5. Likelihood-Ratio Test and Wald Test scores for six-variable and five-variable models.

	6 VM	6 VM (TROOT)	6 VM (TREE)	6 VM (SQD2BA)	6 VM (DENBA)	6 VM (D2BA)	6 VM (AVDBH)
LL(N)	-362.9747	-373.2817	-373.8965	-372.4245	-380.3584	-367.0950	-366.3463
LL(O)	-469.9469	-469.9469	-469.9469	-469.9469	-469.9469	-469.9469	-469.9469
LR Test Null	213.9444	193.3303	192.1008	195.0448	179.1770	205.7037	207.2010
p-value	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
LR Test (5v6)	---	20.6141	21.8436	18.8996	34.7674	8.2407	6.7433
p-value	---	0.0000	0.0000	0.0000	0.0000	0.0041	0.0094
Wald Test	---	17.2436	18.3493	22.3193	24.3344	22.8239	5.9872
Wald prob.	---	0.0000	0.0000	0.0000	0.0000	0.0000	0.0144
Rho-Squared*	0.2276	0.2057	0.2044	0.2075	0.1906	0.2189	0.2205
Correct Response	0.4469	0.4275	0.4266	0.4295	0.4282	0.4392	0.4440
Correct Reference	0.8015	0.7945	0.7942	0.7952	0.7948	0.7987	0.8004
Total Correct	0.7078	0.6976	0.6971	0.6986	0.6979	0.7038	0.7063

*McFadden's Rho-Squared

Table 6. Six-variable model.

$$E(Y_i)=\pi_i=\frac{\exp\left(\beta_0+\beta_1\bullet\sqrt[3]{\frac{dbh\bullet din}{ba}}+\beta_2\bullet\frac{dbh}{msasbingdbh}+\beta_3\bullet\sqrt{\frac{dbh^2}{ba}}+\beta_4\bullet\left(\frac{inden}{ba}\right)\left(\frac{oden}{ba}\right)+\beta_5\bullet\frac{dbh^2}{ba}+\beta_6\bullet SAdbh\right)}{1+\exp\left(\beta_0+\beta_1\bullet\sqrt[3]{\frac{dbh*din}{ba}}+\beta_2\bullet\frac{dbh}{msasbingdbh}+\beta_3\bullet\sqrt{\frac{dbh^2}{ba}}+\beta_4\bullet\left(\frac{inden}{ba}\right)\left(\frac{oden}{ba}\right)+\beta_5\bullet\frac{dbh^2}{ba}+\beta_6\bullet SAdbh\right)}$$

dbh is diameter at breast height; din is diameter increment measured at breast height; ba is stand basal area; inden is ingrowth density; oden is overstory density; SAdbh is stand average dbh – See Table 1 for further information.

where

- $E(Y_i)$ – is the *E*xpected Y_i
- Y_i – is the binary response (0 = survival, 1 = dead)
- π_i – is the probability associated with the expected response
- exp – is the natural logarithm (2.728281...)
- β_0 – is the constant for the model
- $\beta_1 \ldots \beta_6$ – are the coefficients for each variable
- and the variables are as explained in Table 1.

Table 7. Coefficient estimates for the six variables and the Constant of the six-variable model.

Variable	Estimate
Constant	3.15309
TROOT	-4.07188
TREE	2.68940
SQD2BA	-12.37235
DENBA	-0.000116
D2BA	5.57408
AVDBH	-0.12754

In Table 8 Response refers to instances of mortality (1's) and Reference refers to instances of survival (0's).

Table 8. Prediction success table for the selected six-variable model.

		Predicted Choice		
		Response	Reference	Actual Total
Actual Choice	Response	96.08	118.92	215
	Reference	118.92	480.08	599
	Prediction Total	215	599	814
	Correct	0.447	0.801	
	Total Correct	0.708		
	Sensitivity	0.447		
	Specificity		0.801	
	False Reference	0.553		
	False Response		0.199	
	Success Index	0.183	0.066	

The odds ratios and the confidence interval for each variable in the six-variable model are presented in Table 9. The odds ratios indicate that each variable significantly affects the odds ratio within the model. The odds ratio for a variable is the multiplicative factor by which the odds $\left(\frac{\pi_i}{1-\pi_i}\right)$ change when the independent variable increases by one unit.

Table 9. Odds Ratios.

Variable	Odds Ratio	95 % Bounds	
		Upper	Lower
TROOT	0.0170	0.1165	0.0025
TREE	14.7229	50.3974	4.3011
SQD2BA	0.000001	0.0007	0.0000
DENBA	0.9999	0.9999	0.9998
D2BA	263.5073	2593.7900	26.7702
AVDBH	0.8803	0.9749	0.7948

The odds ratio for a variable is significant when the upper and lower confidence interval do not include the number 1.0. When the upper and lower bounds are lower than 1.0, the odds ratio significantly lowers the odds and when it is greater than 1.0, it significantly increases the odds. The odds ratio value for a particular value is partially dependent on the size and magnitude of the variable in question, and a very small or very large odds ratio value does not indicate better or worse performance. For example, the variable SQD2BA has a very small odds ratio value while DENBA has a value very close to 1.0. The smallest value of SQD2BA in the data set (not shown) is 0.1744 while the largest value for SQD2BA in the data set is 1.8462. The spread is not large and the numbers are not large, so a unit change of 1.0 will produce a larger change in the odds than a variable with a larger spread of values. This is reflected in the odds ratio which has a very small number that will result in substantial change in the odds for even a small increase in the odds ratio. DENBA, conversely has a data spread in the data set of 15.7 to 36249.1 (not shown), so both the spread of the data and the size of the numbers is large. A unit change of 1.0 for DENBA will produce a smaller multiplicative change for the odds. This is of course reflected in the odds ratio value of 0.9999 which will

produce only small changes in the odds with a unit change of 1.0 in the independent variable.

Deciles of Risk (goodness-of-fit statistics) are used to make sure that the model fits the data and that the results are not unduly influenced by a few observations. In this procedure 10 categories (bins) from 0 to 1 are developed and the estimated probability for each record is allocated to one of the 10 categories. The size of the categories and the allocation procedure can be determined by the modeller. Two different categories were used in two different deciles of risk analyses. One involved even separation of the categories, which ignored the spread of the data, while the second allocated approximately equal numbers of observations to each category and from this determined the spread size of the category.

For the first deciles of risk table presented in Table 10 the category separation values are equal intervals from 0 to 1 in increments of 0.1. For each category the responses observed and responses expected are listed along with references observed and references expected. The average probability of the predicted probabilities for each observation is included for each bin. Also included as a component of Table 10 are the results of the goodness-of-fit statistics.

Although the Hosmer-Lemeshow Test is the generally preferred test in mortality studies, three goodness-of-fit statistics are provided here for the interested reader. The Hosmer-Lemeshow Test indicates that there are no serious deviations between observed and expected values for the 10 categories. The Pearson, and Deviance goodness-of-fit statistics confirm this. The alternative hypothesis that there are significant differences between observed and expected values for each category is rejected in favour of the null

Table 10. Deciles of Risk with category separations based on equal intervals.

	Statistic	p-value	df
H – L*	10.22	0.25	8
Pearson	765.55	0.85	807
Deviance	725.95	0.98	807

Category	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1
Resp Obs	14	18	27	29	44	30	14	20	18	1
Resp Exp	8.45	24.39	29.58	30.27	41.22	27.8	13.43	23.03	15.92	0.93
Ref Obs	212	147	94	57	49	21	7	11	1	0
Ref Exp	217.55	140.61	91.42	55.73	51.78	23.2	7.57	7.97	3.08	0.07
Avg Prob	0.04	0.15	0.24	0.35	0.44	0.55	0.64	0.74	0.84	0.93
Total O/E	226	165	121	86	93	51	21	31	19	1

*Hosmer-Lemeshow
Resp Obs – Responses Observed (1's = mortality)
Resp Exp – Responses Expected (according to the model)
Ref Obs – Reference Observations (0's = survival)
Ref Exp – References Expected (according to the model)
Avg Prob – Average Probability (The average probability of the observed values in the category)
Total O/E – The total number of values in the category (either observed or expected)

hypothesis for all three tests. The p-value for each test is greater than or equal to 0.25, which is much larger than the cut-off of 0.05.

Table 10 is heavily skewed in favour of the lower decile categories. Almost 28% of the predictions fall in the first category interval (0 – 0.1) and only one prediction falls in the final category interval (0.9 – 1.0). The declining trend from zero to one would tend to indicate that trees are either obvious survival trees, or they are closer to the middle of the zero-one probability interval. A further consideration in future research could be given to whether or not the cut- off value of 0.5 is the suitable value or if there is a better 'optimal' value.

Table 11. Deciles of Risk based on equal counts per category.

	Statistic	p-value	df
H – L*	8.58	0.38	8
Pearson	765.55	0.85	807
Deviance	725.95	0.98	807

Category	0.013	0.058	0.112	0.155	0.213	0.275	0.368	0.442	0.577	1
Resp Obs	0	5	10	10	15	12	28	31	45	59
Resp Exp	0.64	2.67	6.6	11.11	14.91	19.23	26.37	30.55	43.74	59.18
Ref Obs	79	78	68	74	67	69	54	44	43	23
Ref Exp	78.36	80.33	71.4	72.89	67.09	61.77	55.63	44.45	44.26	22.82
Avg Prob	0.01	0.03	0.08	0.13	0.18	0.24	0.32	0.41	0.5	0.72
Total O/E	79	83	78	84	82	81	82	75	88	82

*Hosmer-Lemeshow

The second deciles of risk table (Table 11) uses equal counts (observations) per bin, although the count is an approximation. The category separator values are determined from the observations. This second deciles of risk table is presented to see if the equal interval method of the previous tables has produced erroneous results. The advantage to assigning an approximately equal number of observations to each bin is that it allows the variability inherent to the data to be expressed within the test. As seen in Table 11 the probability values for each observation are closer to 0 than to 1 (obviously there are many more observations of survival than of mortality). The ninth category contains response values whose probability is greater than 0.442 and less than or equal to 0.577, while the tenth category contains variables between 0.577 and 1.0. Since each bin contains roughly an equal number of observations, it is possible to see in Table 11 that the data are not uniformly distributed between 0 and 1.0. For this reason including the second deciles of risk table is warranted to ensure that no one table is chosen to mask significant test results and to ensure that the variability of the data does

not preclude observations of poor fit. The goodness-of-fit statistics (Tables 10 and 11) fail to reject the null hypothesis and it is concluded that there are no significant differences between the observed and the expected values.

4.2 GRAPHICAL EXAMINATION OF THE RESIDUALS

In this section, residuals of the developed model are examined to determine if there are any influential outliers, and to determine if the model is adequate. Four types of residuals are calculated and examined for such purposes (Ordinary residuals, Pearson residuals, Studentized Pearson residuals (also called Standardized Pearson residuals), and Deviance residuals. Because residuals can take on only one of two values, those predictions that are mortality observations are positive numbers and survival observations are negative numbers.

Four graphs of residuals plotted against estimated probabilities are presented with Lowess Smooth Lines added (Figures 1, 2, 3 and 4) to examine the residuals for outliers. A Lowess smooth line uses a weighted average for a span of data to indicate potential trends in the data.

As is evident in Figure 1, showing ordinary residuals plotted against estimated probability, there are two linear trends of residuals with each line of residuals having a slope of -1. For logistic regression, as already discussed, the residuals can take on only one of two values at any given point, either $1-\hat{\pi}_i$ or $0-\hat{\pi}_i$ (Steinberg and Colla 2005). Similar patterns are seen in Figures 2, 3 and 4. The residuals seen in those figures are calculated in a different manner than ordinary residuals (see Kutner et al. 2005, Steinberg and Colla 2005). One obvious deviation for the Studentized Pearson

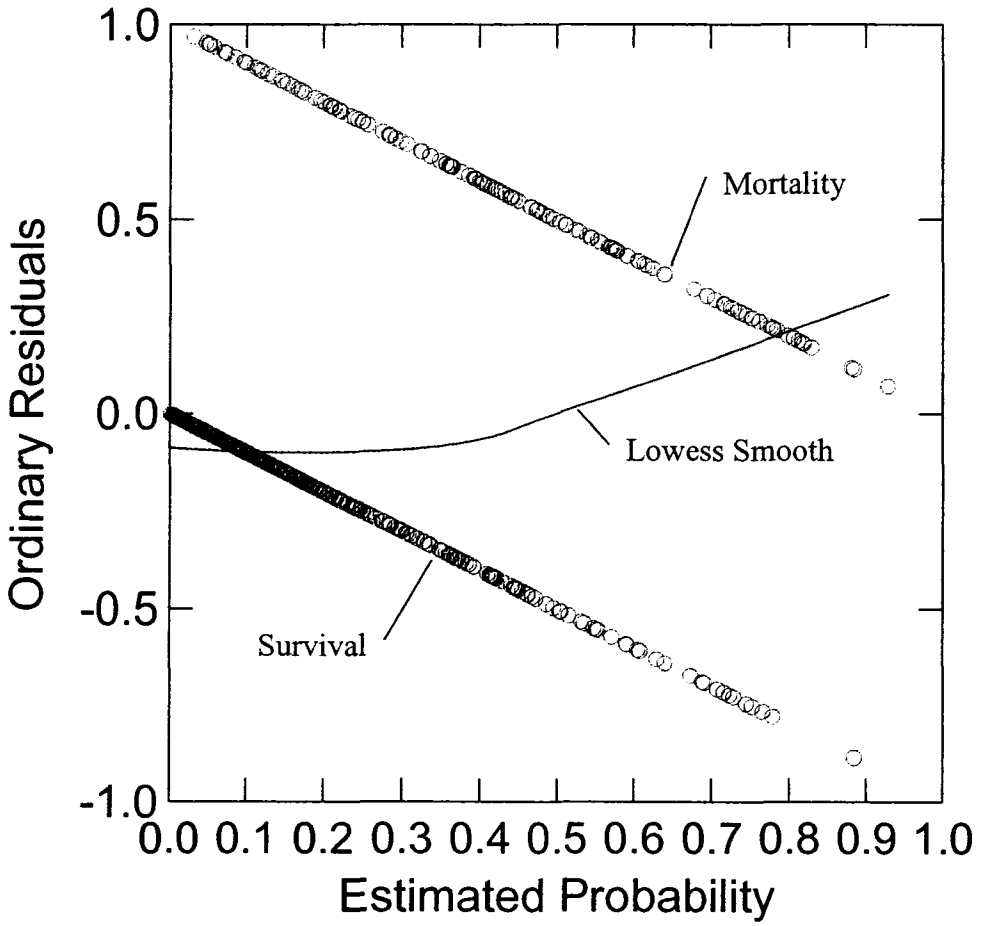

Figure 1. Ordinary residuals against estimated probabilities with Lowess Smooth (cut-off value of 0.5).

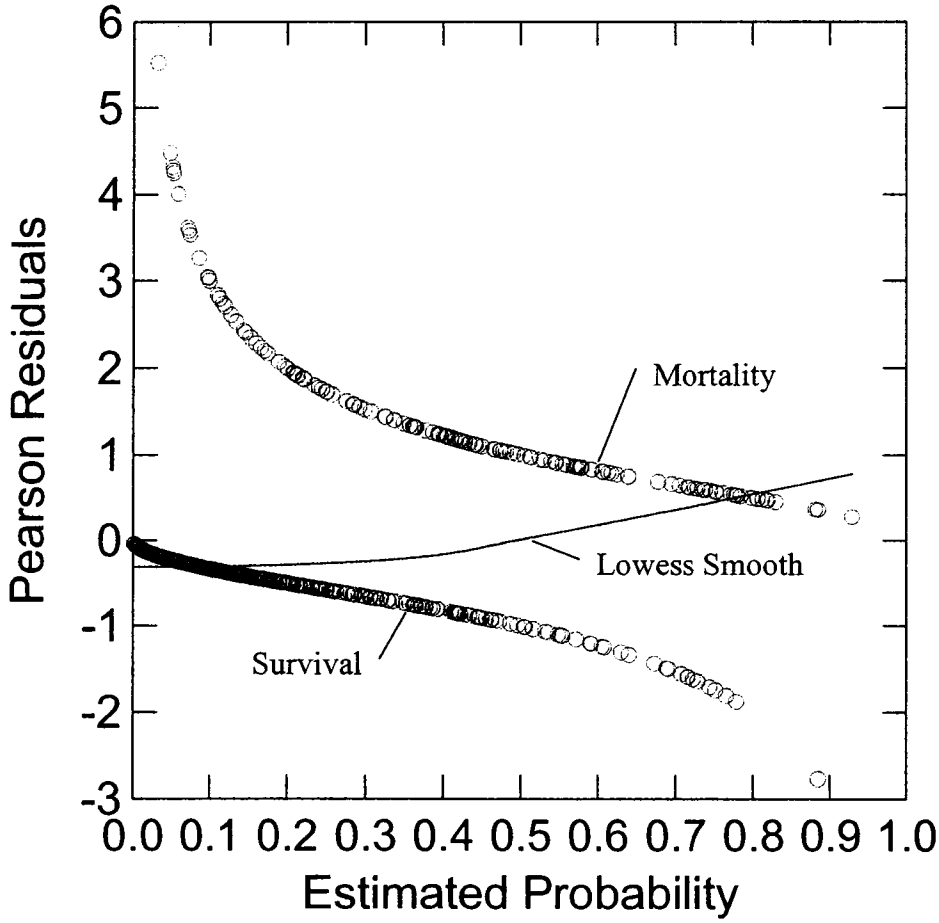

Figure 2. Pearson residuals against estimated probabilities with Lowess Smooth (cut-off value of 0.5).

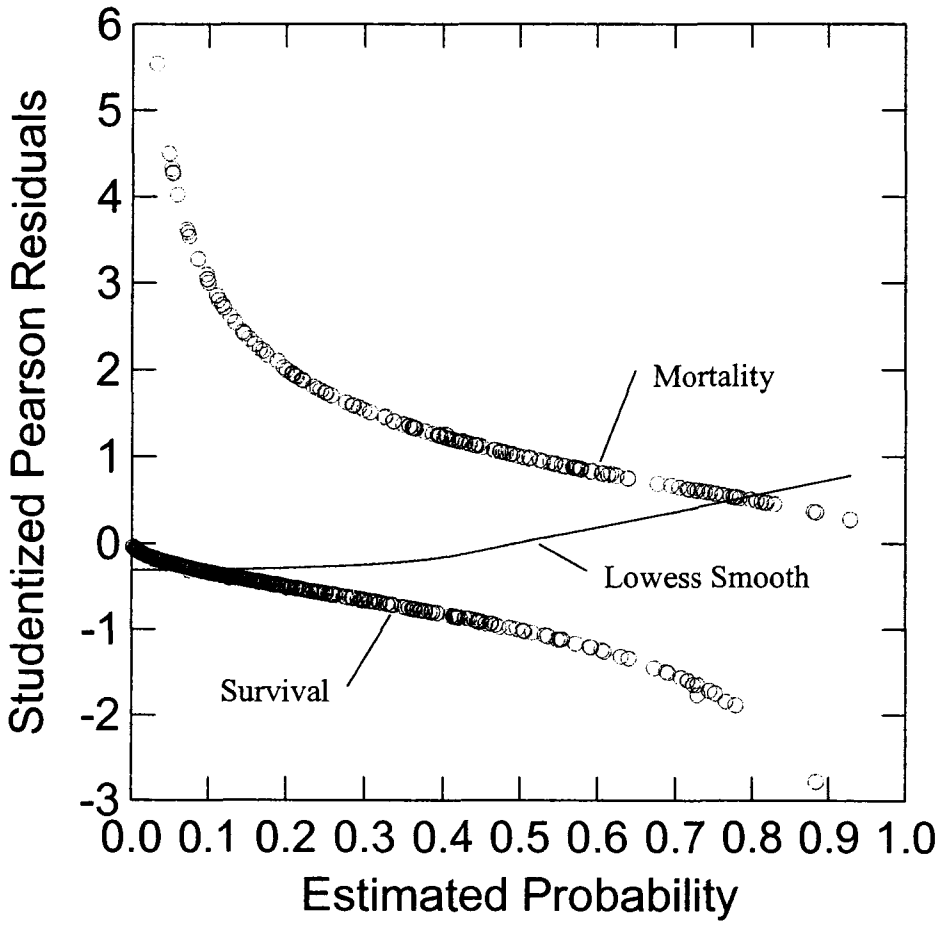

Figure 3. Studentized Pearson residuals against estimated probabilities with Lowess Smooth (cut-off value of 0.5).

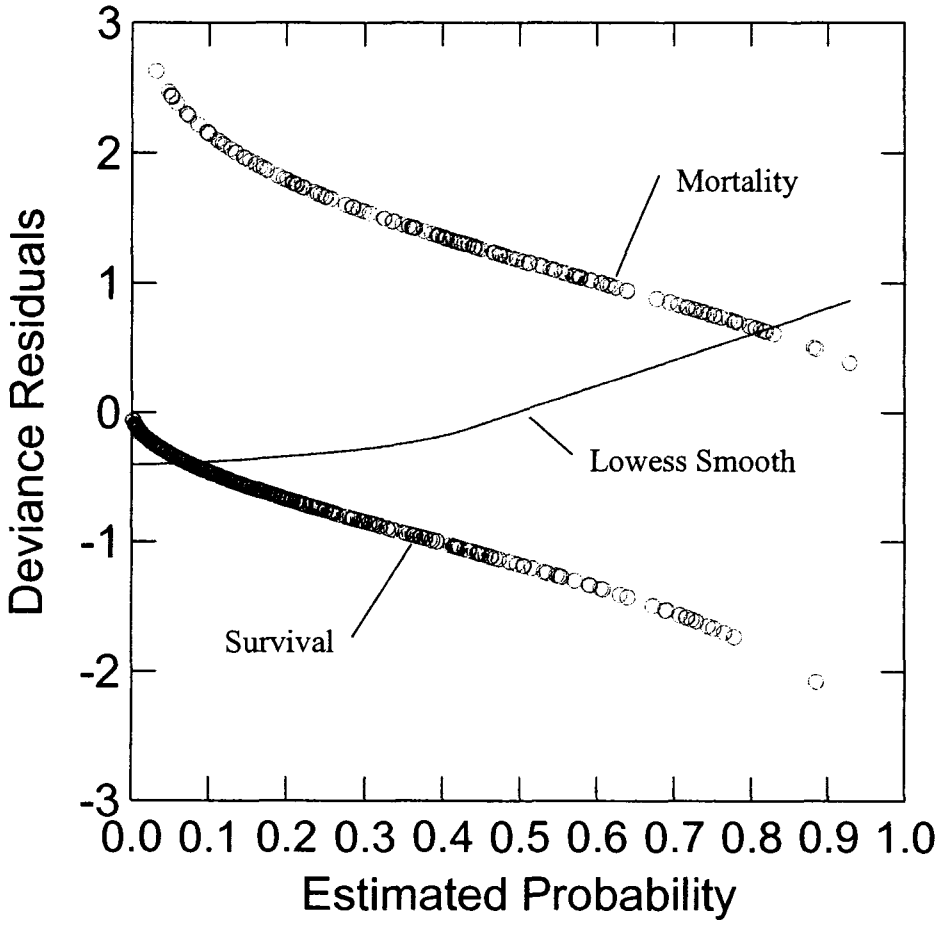

Figure 4. Deviance residuals against estimated probabilities with Lowess Smooth (cut-off value of 0.5).

Residuals versus the Pearson Residuals (Figure 2 versus Figure 3) occurs in the incorrect survival area with an estimated probability of about 0.725 and a Studentized Pearson Residual of about −1.75. It appears as a deviation from the observed trend. The reason for the deviation is unknown as is the importance of the deviation.

In ordinary regression, residual plots are useful for diagnosing model inadequacy, non-constant variance, and the presence of outliers. However, in logistic regression, in general, only detection of model inadequacy is pursued (Steinberg and Colla 2005). Thus, detection of outliers is a difficult task in logistic regression.

A Lowess smooth of the plot of the residuals against the estimated probability (or against the linear predictor) should result in an approximately horizontal line with zero intercept, with any significant departure suggesting an inadequate model (Steinberg and Colla 2005). In each of the four graphs the upper linear trend is the mortality residual trend and the lower linear trend is the survival residual trend and the nearly horizontal line is the Lowess Smooth Line.

Also appropriate is to plot the same four types of residuals against the linear predictor. For graphs of residuals against the linear predictor see Appendices I, II, III and IV. The linear predictor is simply $\hat{\pi}_i'$ where $\hat{\pi}' = \log_e\left(\frac{\hat{\pi}}{1-\hat{\pi}}\right)$. Although not discussed further, the four graphs of residuals against the linear predictor produce mildly convex curves, which are similar to the graphs plotted against the estimated probability. They too do not warrant a conclusion of model inadequacy.

The graphs presented in Figures 1, 2, 3 and 4 do not provide any conclusive reasons for eliminating an observation. That is to say there are no observations that can conclusively be declared outliers. Each Lowess Smooth line is approximately horizontal. Deviation from horizontality occurs where there are fewer observations, likely permitting the line curve. Figures 1 through 4 indicate that the model is adequate and that there are no outliers.

In order to further examine the possibility of problematic outliers, two graphs are presented (Figures 5 and 6). The first is change in Pearson Chi-Square values (called DELPSTAT in Systat). These are plotted against estimated probabilities and are shown in Figure 5. The linear trend that begins high on the y-axis and decreases as it progress along the x-axis are mortality predictions. The other linear trend is survival predictions.

It can be seen from this graph that there are potentially some outliers as seen by the very large deviation values given by the Pearson Chi-Square value on the left side of the graph in the range of very small probability values. There is also, potentially, an outlier on the right hand side of the graph with an estimated probability value a little smaller than 0.9. To see if the residuals with a large y-axis value are in fact outliers the model input data is modified by first eliminating the largest DELPSTAT value in the input data set and then by eliminating all DELPSTAT values greater than 10. This procedure was followed by re-estimating the DELPSTAT values and re-graphing residuals at each iterative stage of observation elimination. At each successive iteration of residual removal, model fit improved and in some cases dramatically. Also, the log-likelihood value increased substantially which is commensurate with expectations for an increasing fit statistic, however, the prediction success table did not indicate more correct predictions were made. The prediction success table indicated that the proportion of

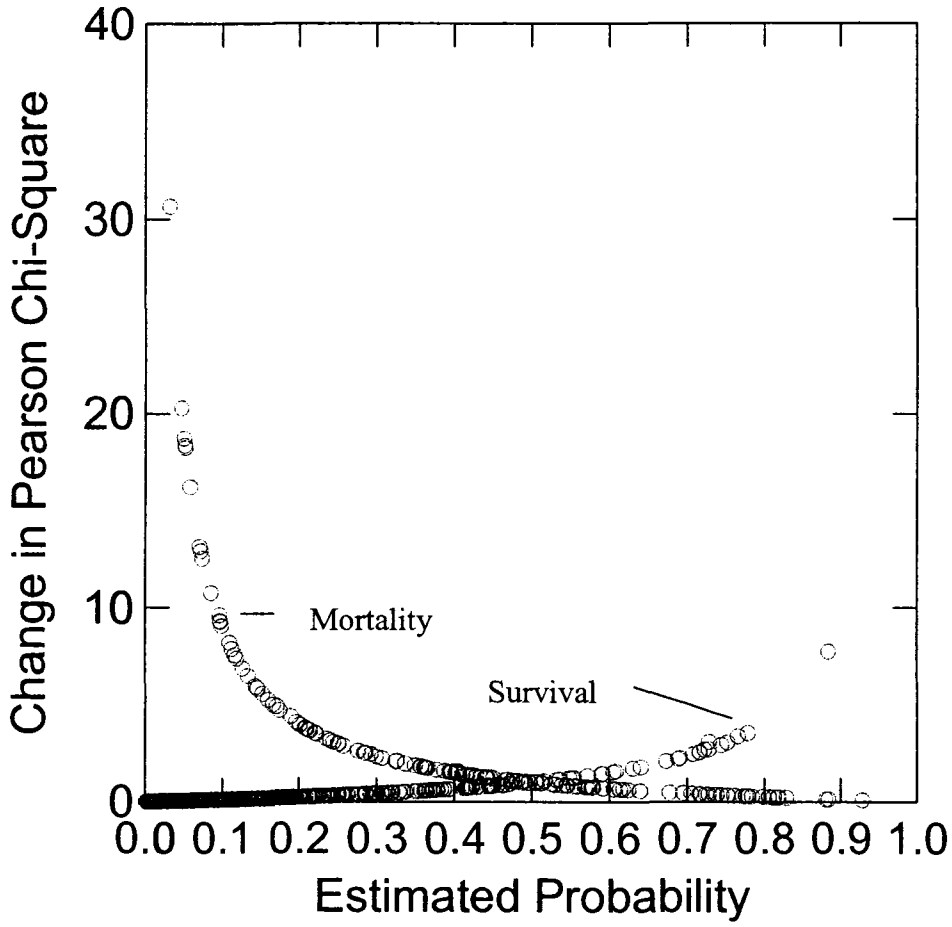

Figure 5. Change in Pearson Chi-Square plotted against the estimated probability.

correct predictions increased but the absolute number of correct predictions remained unchanged. The explanation for this is that elimination of observations led to a model that was over-parameterized (Penner 2006 pers. comm.). To further examine data for outliers a second graph was produced to examine residuals. Figure 6 is change in deviance residual values plotted against estimated probability. Figure 6 has two trend lines, each line increases at a steady rate towards the extreme end values of the probability distribution (0 and 1). Figure 6 does not show any particular necessity for eliminating observations as the residuals are evenly distributed.

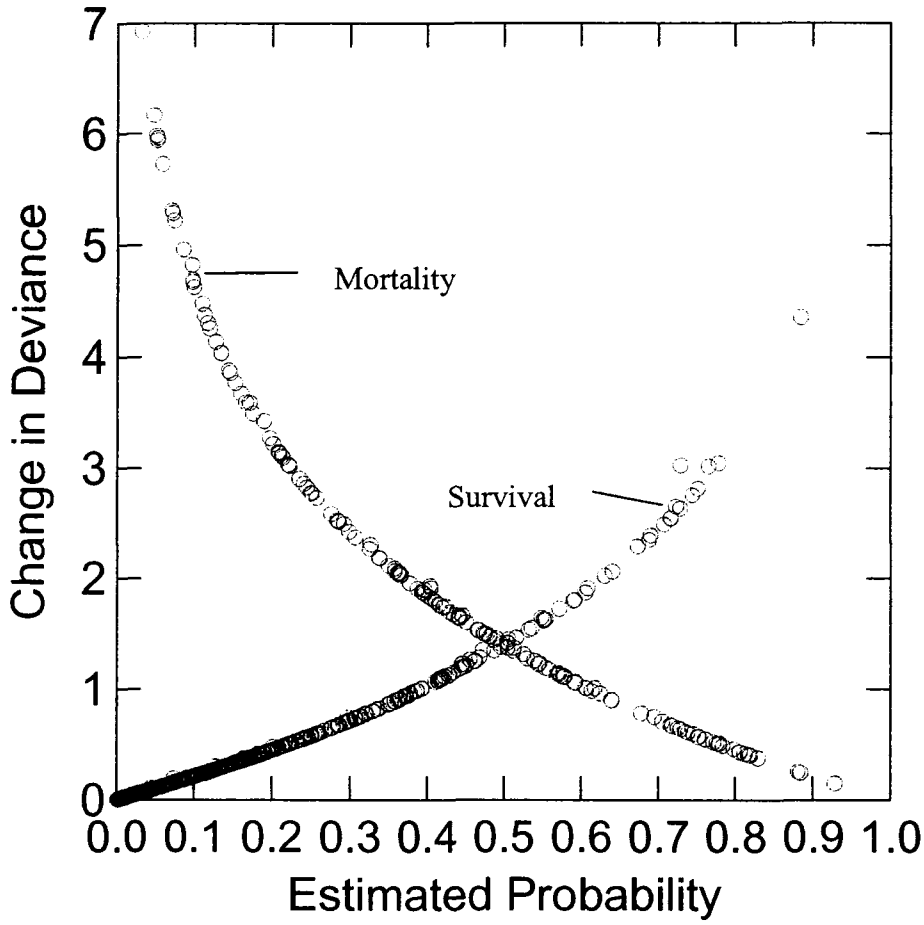

Figure 6. Change in Deviation plotted against the estimated probability.

As a last examination of residuals, a graph of Hadi's Influence Index plotted against Studentized Pearson Residuals, with which the Index was constructed, was developed as shown in Figure 7. This graph shows both the potential of a point to influence the regression (related to its leverage) and a studentized residual, which indicates whether the point exercises its potential (Velleman 1988). Points found near either axis are not influential, while those found in the upper right quadrant of the display are considered to be strongly influential.

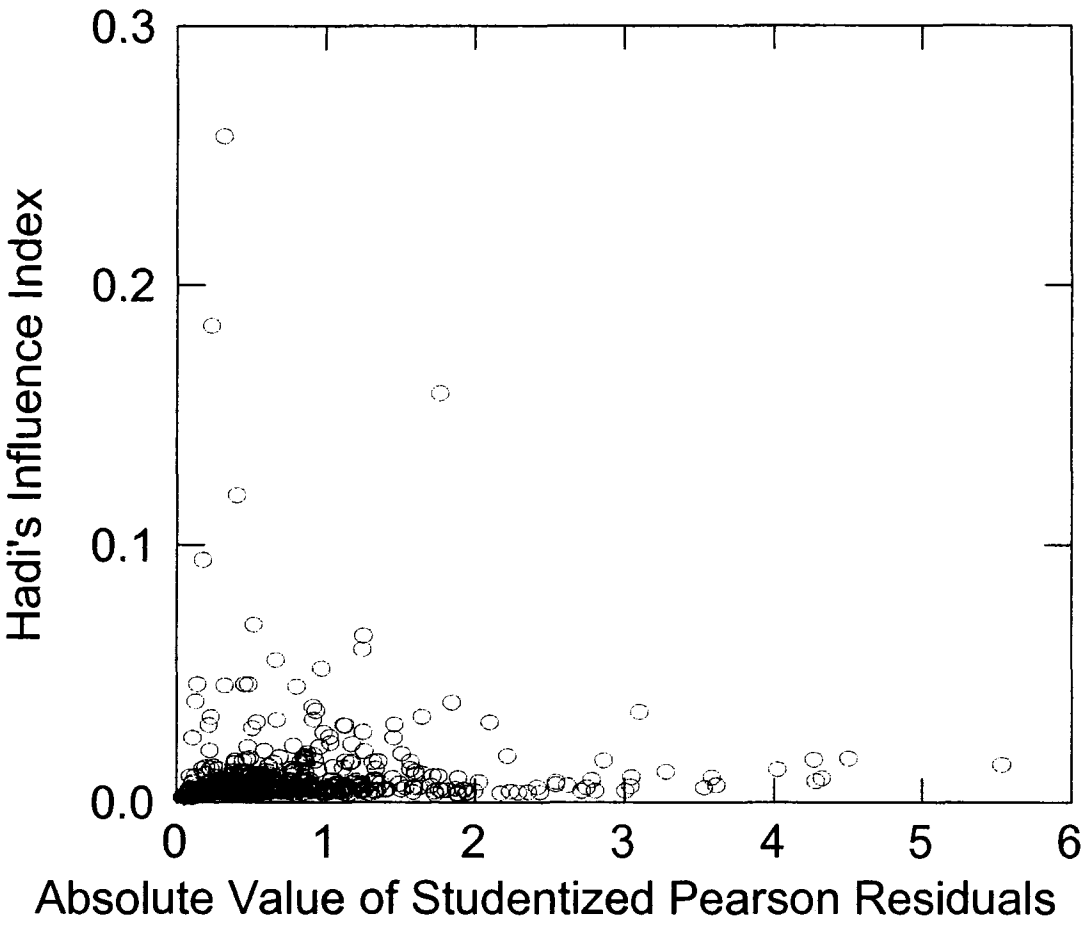

Figure 7. Hadi's Potential Residual Plot for Studentized Pearson residuals.

Hadi's Influence Index was calculated using the leverage equations found in Hosmer and Lemeshow (2000) and the Studentized Pearson Residuals. No points appear to be highly influential. The observation located at approximately x = 1.75 and y = 0.16 when removed as an observation from the data set had no effect on the model residuals, and was, therefore, retained as a component of the model. Because three separate graphs indicated no outliers, no further examination of residuals for outliers was conducted, and the data set was left intact with no observations removed.

As a final step in graphically analysing the data, two final graphs are produced. The first is estimated probabilities plotted against expected value for a normal distribution (Figure 8), and the second is estimated probabilities plotted against linear predictors (Figure 9). As can be seen for both Figures 8 and 9, estimated probabilities are both sigmoidal and monotonic.

Figure 9 is similar to Figure 8. The upper and lower tails, of Figure 9 are perhaps more representative of the actual distribution of observations. Figure 8 shows

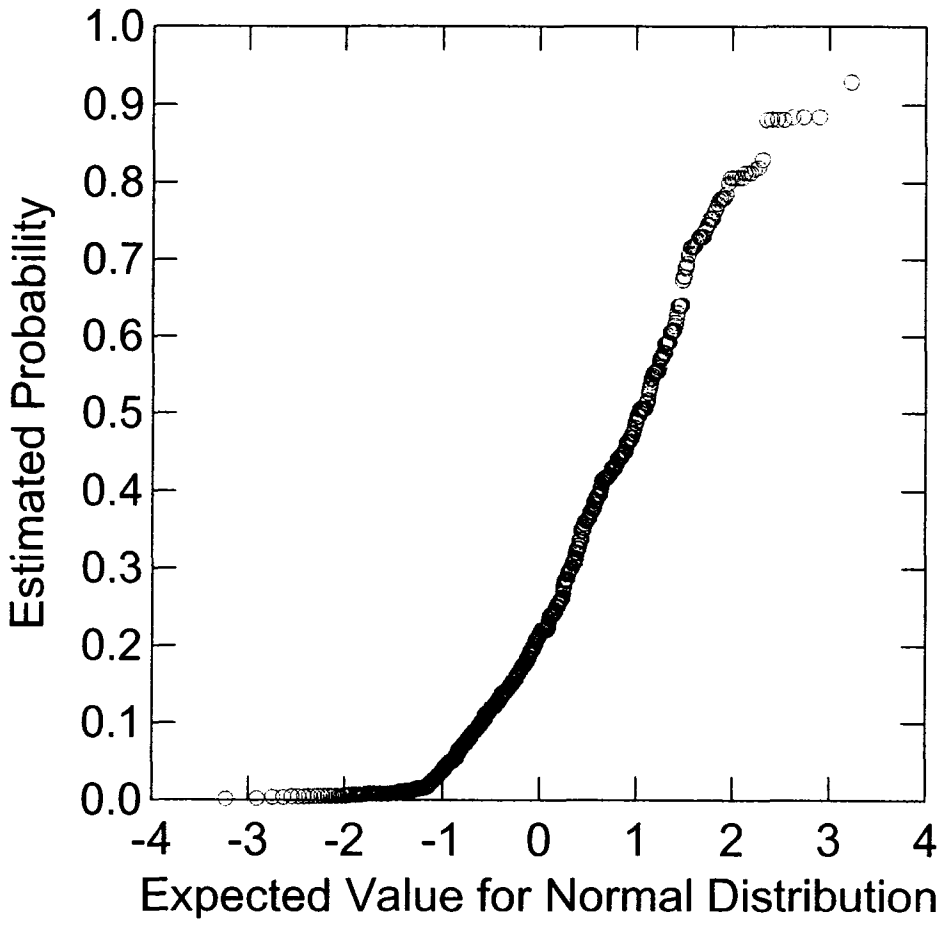

Figure 8. Estimate Probabilities against expected values for the Normal Distribution.

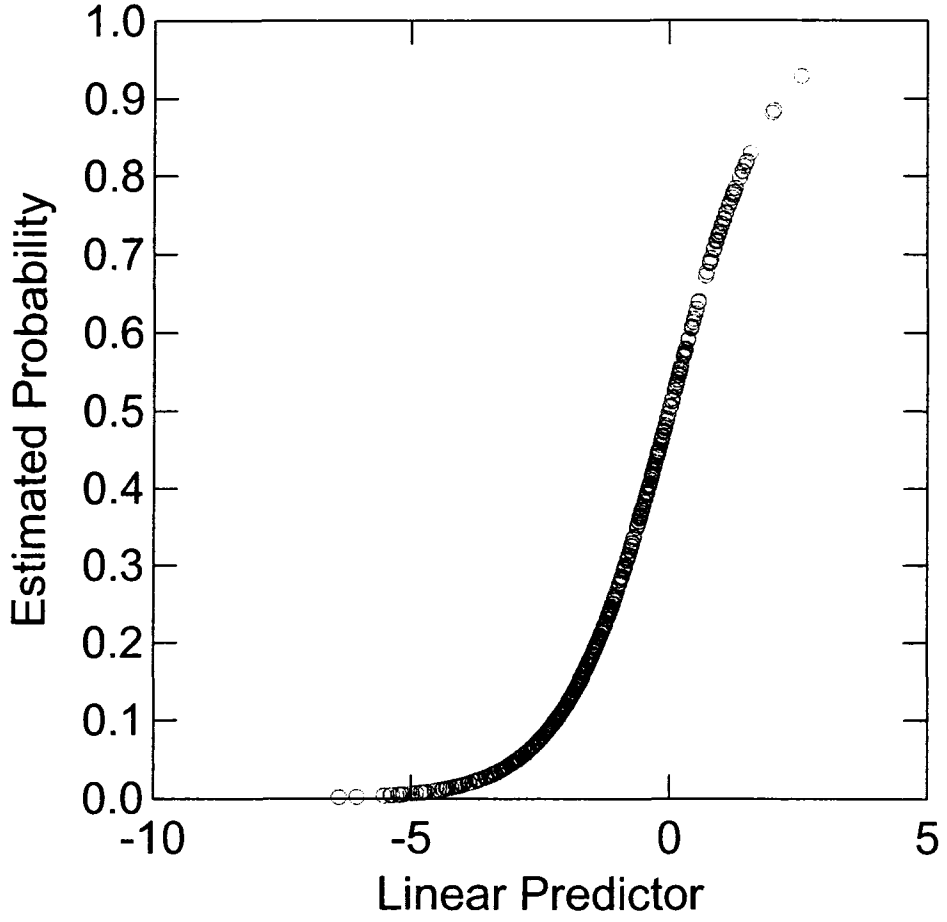

Figure 9 Estimated Probability against Linear Predictor.

that there is a long tail in the lower probability range that almost touches zero. In the upper probability range the tail becomes separated, and fails to reach the upper limit of one. This is potentially a result of fewer observations of mortality and some mild disparity surrounding the calculation of parameters based on the available data. No problems are perceived from the shape of Figure 8. Finally in regard to Figure 8, it should be noted that it is almost linear between the tails as it is predicted to be.

4.3 RESULTS OF MODEL USE WITH AN INDEPENDENT DATA SET

An independent data set was used with the developed model to see how the model performs with data other than the developmental data. Because the independent data set did not contain identical information a direct test of the model was not possible. Instead, several modifications to the independent data set were made and are described below.

The independent data set (see Methods and Materials) used to examine the developed model had two deficiencies. First was an inability to extract ingrowth data from the data set. A second problem was an inability to calculate the necessary variables. The data shortcomings affected two variables (TREE and DENBA) in particular. The variable TREE (see Table 1) requires average black spruce understory ingrowth diameter at breast height (*avsbingdbh*), and DENBA (see Table 1) requires understory ingrowth density of black spruce.

In the first instance, a decision was made to use all black spruce classifiable as understory, but not necessarily ingrowth understory. This was done by examining average diameter at breast height for all trees in a stand and average diameter at breast height for all black spruce trees in a plot. If average tree size was small (e.g., < 10 cm) the entire stand was eliminated from consideration under the contention that it was a juvenile stand. The primary potential shortcoming, and, therefore, risk to the test, was that it might be possible for highly suppressed individuals to be a component of the test data, because trees did not have to grow into the plot, they merely had to be smaller individuals. In the developmental data set the trees had to grow into the plot and were therefore unlikely to be suppressed individuals of the original stand.

Second, input variables were changed to provide approximate, albeit relative, relations between data. The TREE variable was modified in two ways. The first was by using average black spruce dbh for the stand in place of average understory ingrowth dbh (*avsbingdbh*) and then by using the square root of average black spruce dbh for the stand. Since *avsbingdbh* can be difficult to calculate it does not seem unreasonable to use a whole stand measurement instead of a structural component of a stand as a means of testing the model or indeed as a component of a model.

The variable DENBA was also modified. The initial modification involved using black spruce density for the whole stand instead of understory ingrowth density. It was also modified by dropping the component involving understory ingrowth density divided by basal area and only retaining that portion of the variable using total stand density divided by basal area.

The primary argument regarding validity of modifying the input data and variables, as a suitable method, is that it does not drastically alter the model being tested and the data are similar in scope to the developmental data. It also approximates a data selection procedure that might be taken for validating a model developed based on broad diameter classes (e.g. 5 cm or 10 cm classes), or a model developed based on below average tree size for either the stand or the species. Pursuant to the above process, data used in the test was also limited to the same size range (dbh) as the model development data (in this case only trees less than or equal to 8.3 cm in diameter at breast height were eligible because 8.3 cm was the largest tree in the development data). All other variables such as diameter increment, basal area, average dbh and density remained unrestricted in their range even if it exceeded that of the development data set. Stands used in testing were still required to be mixed species stands.

A direct test of the model with an independent data set was not possible, as stipulated above. The alternative as presented here is a modified data set used as a proxy to the data. The result of the above modifications was four variants of the independent data set. Var1 uses proxies of the missing data for TREE and DENBA. In the case of the TREE variable, average black spruce dbh was used instead of average black spruce understory ingrowth dbh. For the DENBA variable, total black spruce density was used in place of ingrowth black spruce density. Var2 uses a TREE variable with the square root of average black spruce dbh in the denominator. The DENBA variable remained as in Var1. Var3 used the TREE variable outlined in Var1 while DENBA used total stand density divided by total stand basal area. Var4 used the modified TREE variable as described in Var2 and the modified DENBA variable as described in Var3.

The next step was to take the four data variants and make predictions about mortality or survival using the initially developed model and the estimated coefficients. The results are shown in Table 12, which provides information on how well or how poorly the developed model works on an independent data set.

The first four rows in Table 15 list the number of correct and incorrect mortality and survival predictions. The fifth row labelled total correct is a count of correct mortality and survival predictions, while the sixth row labelled total incorrect is a count of incorrect mortality and survival predictions. The eighth row labelled correct mortality percentage is the percentage of correct mortality predictions. Likewise, the ninth row labelled correct survival percentage is the percentage of correct survival predictions. The final row (Total Correct %) lists the percentage of total correct predictions for both survival and mortality.

Table 12. Prediction results made using developed model for four data variants.

	Var1	Var2	Var3	Var4
Correct Mortality Count	2	217	5	279
Correct Survival Count	1201	859	1200	796
Incorrect Mortality Count	953	0	0	0
Incorrect Survival Count	1	1081	952	1082
Total Correct	1203	1076	1205	1075
Total Incorrect	954	1081	952	1082
Total Predictions	2157	2157	2157	2157
Correct Mortality %	0.21	22.7	0.5	29.2
Correct Survival %	99.9	71.5	99.8	66.2
Incorrect Mortality %	99.8	0.0	0.0	0.0
Incorrect Survival %	0.08	89.9	79.2	90.0
Total Correct %	55.8	50.0	55.9	49.8

Var1 and Var3 have a low number of correct mortality predictions. Both Var1 and Var3 have the highest correct survival predictions possibly because they fail to predict mortality. Var2 and Var4 have the highest correct mortality predictions with 22.7% and 29.2% respectively. Those two variants also have the lowest correct survival predictions with 71.5% (Var2) and 66.2% (Var4). What can be seen from these results is that the model form is capable of being transferred to a different data set.

The developed model had a correct mortality prediction rate of 45%, while the best variant has a correct mortality rate of 29.2%. Var2, Var3 and Var4, have zero instances of incorrect mortality predictions. All of the variants except Var1 have a high percentage of incorrect survival predictions. It is obvious from this that further testing of the model needs to take place in order to determine how to improve its predictive ability.

5.0 CONCLUSIONS AND RECOMMENDATIONS

5.1 CONCLUSIONS

This thesis focused on modelling mortality of understory ingrowth black spruce trees in mixed species stands of Boreal Northern Ontario. Objectives were to develop a mortality model capable of predicting mortality of understory ingrowth black spruce trees in mixed species stands of the boreal forest and to improve understanding of forest stand dynamics in mixed species stands.

The mortality results obtained in this thesis are comparable to other mortality studies in the literature. This study had 45% correct mortality and 71% correct survival predictions for the development data, and 23% and 30% correct mortality predictions and 72% and 66% correct survival predictions for the independent data set (Var2 and Var4). Bigler and Bugmann (2003) achieved 80% total correct classification and 71-81% correct mortality classification for a Norway spruce *(Picea abies* (L.) Karst) mortality model. In a study by Dobbertin and Brang (2001) 33% of the dead trees were correctly predicted to die in the calibration data set and 57% in the validation data set. Monserud (1976) developed a mortality model that was able to correctly classify 88% of the live trees and 35% of the dead trees. Dobbertin and Biging (1998) used a classification and regression tree (CART) to model mortality. They achieved 28-36% mortality prediction accuracy for ponderosa pine (*Pinus ponderosa* Dougl. ex Laws.) and 11-17% mortality predication accuracy for white fir (*Abies concolor* (Gord &

Glend.) Lindl. ex Hildebr.). Although, the predictive results of this particular modelling effort have produced results as good or better then those found in the literature, more work is needed. An extension of this thesis could include the development of better variables, the acquisition of more data, and more rigorous testing of the developed model.

Two variables were used in an attempt to explicitly model stand structure as a component of a mortality model. One variable in particular, TREE, which relates tree size to the average size of other trees in a similar structural location, was found to be important to predicting mortality. A second variable, DENBA, which relates overstory and understory density and basal area, was found to have some influence on the prediction of mortality. From the model results and the two variables mentioned above it can be seen that further examination of stand structure as a component of predicting and explaining black spruce mortality is warranted.

5.2 RECOMMENDATIONS

A question which is suitable for further research, is whether or not the measurements of life and life processes are the most suitable for predicting mortality, or are there better measures of death? Is it possible to directly measure regular and irregular mortality?

As an aid to viewing and detecting mortality, delineation of stand structures, such as understory and ingrowth, or saplings and poles, within a complex stand can lead to a greater ability to model mortality. Are multiple models for a single species necessary for complex stands?

Modelling mortality of individuals where cause of mortality is implicit and not explicit, results in development of variables that detect mortality as observable characteristics of individual trees and the system within which they reside. A recommendation for further research efforts is to incorporate the collection of the cause of death in a permanent sample plot system.

The results obtained in this study suggest that the primary problem with detecting mortality is an insufficient quantity of mortality data. This is not to be confused with an insufficient amount of growth and yield data. Rather it refers to a lack of data about causal agents and the point in time at which a tree can be declared dead. For future work the collection of better mortality indicators is recommended as well as the collection and utilization of variables that are more readily available. For example using whole stand average black spruce dbh instead of understory ingrowth average black spruce dbh could improve the ease of model use.

Perhaps the most important recommendation to stem from this thesis would be to improve the model testing stage. A lot can be gained from such an effort. In particular a better understanding variables, their interactions and deficiencies could be achieved. However, the modelling effort, was itself, one of the most important components of the thesis.

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APPENDICES

APPENDIX I

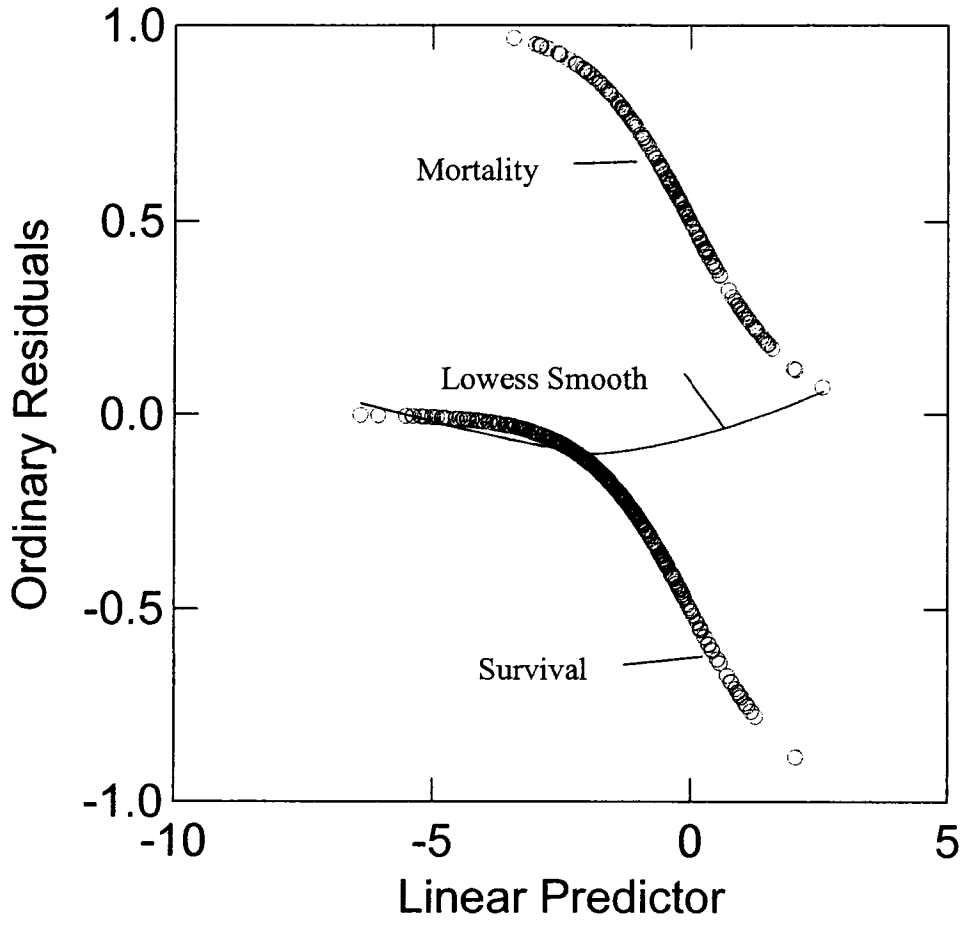

Figure 10. Ordinary Residuals Against Linear Predictor with Lowess Smooth Line

APPENDIX II

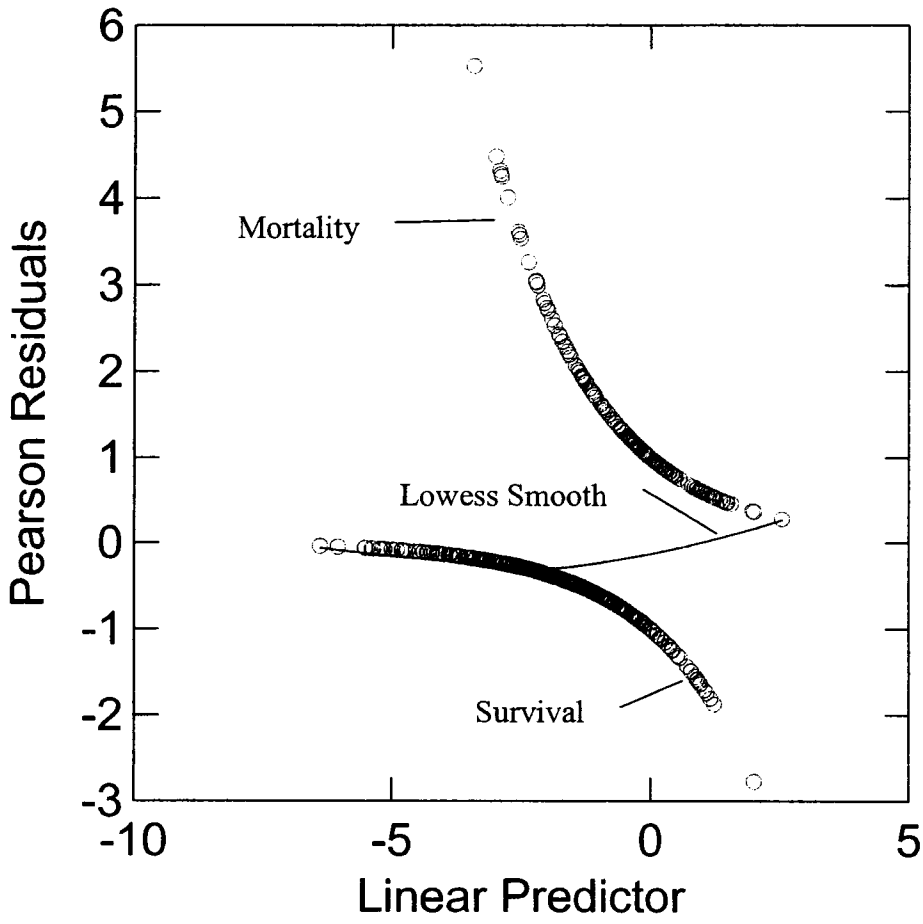

Figure 11. Pearson Residuals Against Linear Predictor with Lowess Smooth Line

APPENDIX III

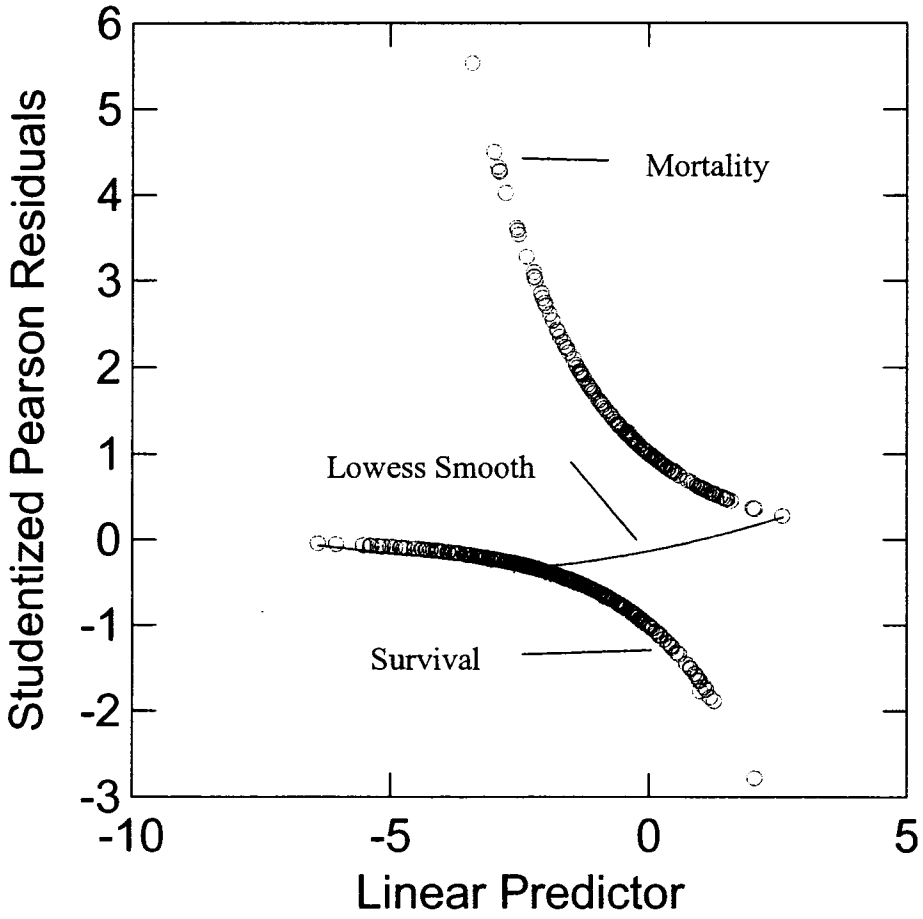

Figure 12. Studentized Pearson Residuals Against Linear Predictor with Lowess Smooth Line

APPENDIX IV

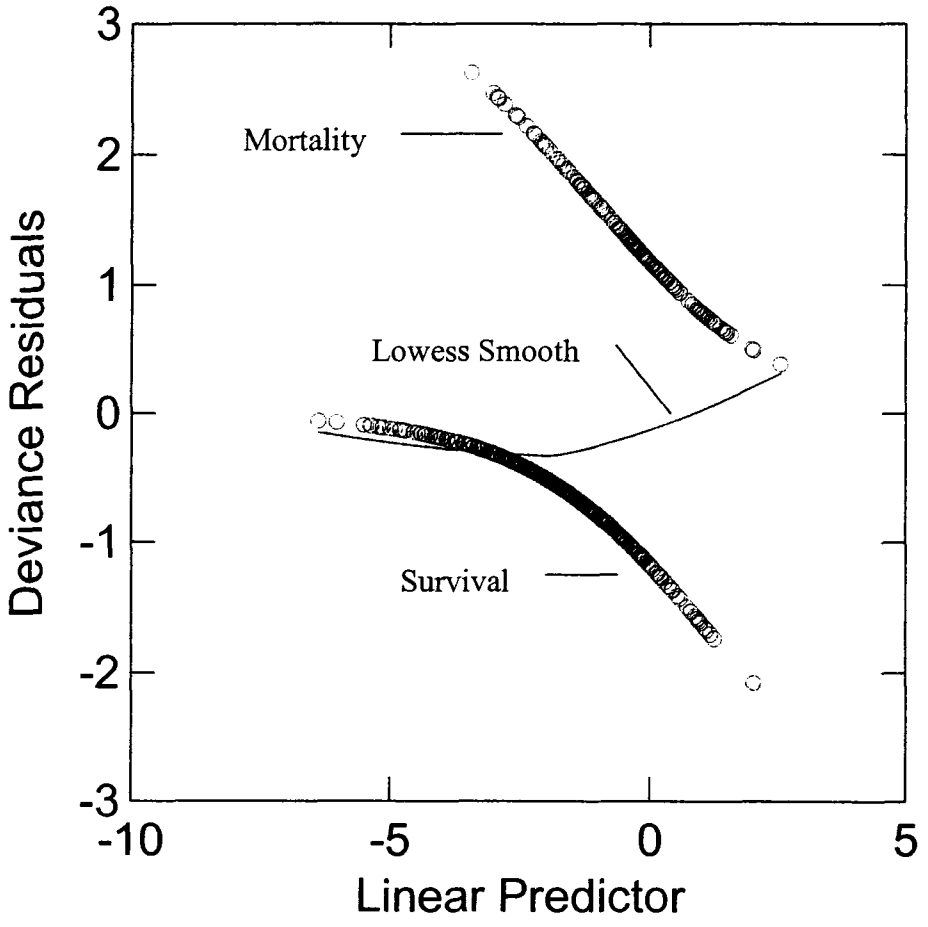

Figure 13. Deviance Residuals Against Linear Predictor with Lowess Smooth Line